

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 ; Search time 52.7808 Seconds
(without alignments)
291.060 Million cell updates/sec

Title: 09782816-1-22

Perfect score: 138

Sequence: 1 EVEKIKTTVKESATREKLPVLAKOLAAI 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: UniProt_sprot:*

2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	400	1	DCT2_HUMAN
2	135	97.8	401	1	DCT2_MOUSE
3	135	97.8	402	1	DCT2_MOUSE
4	114	82.6	338	2	Q6AYH5
5	114	82.6	403	2	Q6AYH5
6	109	79.0	403	2	Q6AYH5
7	92	66.7	405	2	Q6AYH5
8	89	64.5	402	2	Q6AYH5
9	56	40.6	333	2	Q6AYH5
10	54	39.1	445	2	Q6AYH5
11	54	39.1	500	1	C72V_ARATH
12	54	39.1	769	2	Q6BPJ3
13	54	39.1	933	1	GLND_AZOB
14	53	38.4	416	2	Q6BF22
15	53	38.4	710	2	Q6BF22
16	53	38.4	757	2	Q6BF22
17	53	38.4	1373	2	Q6BF22
18	52	37.7	449	2	Q6BF22
19	52	37.7	452	2	Q6BF22
20	52	37.7	470	2	Q6BF22
21	52	37.7	1430	2	Q6BF22
22	51	37.0	131	2	Q6BF22
23	51	37.0	180	2	Q6BF22
24	51	37.0	319	2	Q6BF22
25	51	37.0	378	2	Q6BF22
26	51	37.0	389	2	Q6BF22
27	51	37.0	389	2	Q6BF22
28	51	37.0	389	2	Q6BF22
29	51	37.0	389	2	Q6BF22
30	51	37.0	389	2	Q6BF22
31	51	37.0	389	2	Q6BF22

X=O
K=V
L=I
D=V

ALIGNMENTS

RESULT 1	ID	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE	STANDARD	PRT	400 AA.
AC	Q13561	086YH2; Q9BW17;			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	05-JUL-2004	(Rel. 44, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)				
DE	(p50 dynactin) (DCTN-50) (Dynactin 2).				
GN	Name=DCTN2; Synonyms=DCTN50;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI TaxID=9606;				
RP	[1]	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
RP	MEDLINE=96178072; PubMed=8647893; DOI=10.1083/jcb.132.4.617;				
RT	Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;				
RT	"Molecular characterization of the 50-kD subunit of dynactin reveals				
RT	function for the complex in chromosome alignment and spindle				
RT	organization during mitosis."				
RT	J Cell Biol. 132:617-633(1996).				
RP	[2]	SEQUENCE FROM N.A.			
RP	TISUS-Placenta, Skin, and Uterus;				
RP	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RP	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RP	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,				
RP	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RP	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,				
RP	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,				
RP	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RP	Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,				
RP	Rana S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RP	Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gurnatue P.H.,				
RP	Richards S., Motley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RP	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RP	Fahney J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RP	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RP	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RP	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RP	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,				
RP	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RP	"Generation and initial analysis of more than 15,000 full-length human				
RP	and mouse cDNA sequences."				
RP	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RP	[3]	SEQUENCE OF 1-384 FROM N.A.			
RP	Aumais J.P., Yu-Dee L.-Y.;				
RP	"Human 50 kD dynactin subunit, p50 dynactin, isolated from HeLa				
RP	cells."				
RP	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.				
RP	[4]	SEQUENCE OF 1-13.			

Query Match	Best Local Similarity	Score 138, DB 1, Length 400,
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Pred. No. 1,8e-09;	
1 EYEKIKTVKESATEEKLTPVLAQOLAL 30	115 EYEKIKTVKESATEEKLTPVLAQOLAL 144	
DB		
RESULT 2		
DC2_MOUSE		
ID DCT2_MOUSE STANDARD; PRT; 401 AA.		
AC 099KJ8;		
DT 28-FEB-2003 (Rel. 41, Created)		
DT 05-JUL-2004 (Rel. 44, Last sequence update)		
DT 05-JUL-2004 (Rel. 44, Last annotation update)		
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)		
DE (p50 dynactin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein		
DE 23-48k) (GMP23-48k).		
GN Name=Dctn2;		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX NCBI_TaxID=10090;		
XX [1]		

SEQUENCE FROM N.A.
RX MEDLIN=233862577, PubMed=12477932; DOI=10.1073/pnas.242603899;
RX STRUBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alechuk S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skelstra T., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
[2]
SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,
RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP TISSUE=Brain;
RC MEDLIN=97289622; PubMed=9144527; DOI=10.1006/bhrc.1997.6447;
RX Abbe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.,
RT "The presence of the 50-KDa subunit of dynein complex in the nerve
RL growth cone." ;
RL Biochem. Biophys. Res. Commun. 233:295-299(1997).
[3]
INTERACTION WITH BICD2.
RX MEDLIN=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
RA Hoogenraad C.C., Akhmanova A., Howell S.A., Dortland B.R.,
RA De Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjaard N.,
RT "Mammalian Golgi-associated Bicardal-D2 functions in the dynein-
RT dynein pathway by interacting with these complexes." ;
RL EMBL J. 20:4041-4054(2001).
CC -I- FUNCTION: Modules cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in synapse formation
CC during brain development.
CC -I- SUBUNIT: Subunit of dynein, a multiprotein complex associated
CC with dynein (BY similarity). Interacts with BICD2.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC -I- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic
CC and membrane-associated forms in neonates. Levels of membrane-
CC associated form are greatly reduced in the adult.

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DR EMBL; BC0004613; AAH04613.1; -
DR MGD; MGI:107733; Dctn2.
DR InterPro; IPR006996; Dynamein.
DR Pfam; PF04912; Dynamein; 1.
KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0 By similarity.
FT DOMAIN 98 131 Coiled coil (potential).
FT 214 244 Coiled coil (potential).
SQ SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940BEC CRC64;

Query Match 97.8%; Score 135; DB 1; Length 401;
Best Local Similarity 96.7%; Pred. No. 4,5e-09;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKITTVESATEEKLTPVLAQKQAL 30
DB 115 EVEKITTVESATEEKLTPVLAQKQAL 144

RESULT 3
ID Q6AYH5 PRELIMINARY; PRT; 402 AA.
AC Q6AYH5;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Dnactin 2.
GN Name=Dcn2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Kozminski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RC Director AGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC079042; AAH79042.1; -
DR GO: GO:0005869; C:dynactin complex; IEA.
DR GO: GO:0007017; P:microtubule-based process; IEA.
DR InterPro: IPR006996; Dnactin.
DR Pfam: PF04912; Dnactin; 1.
SQ SEQUENCE 402 AA; 44148 MW; 550335535A4FB052 CRC64;

Query Match 97.8%; Score 135; DB 2; Length 402;
Best Local Similarity 96.7%; Pred. No. 4.5e-09;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKITTVESATEEKLTPVLAQKQAL 30
DB 116 EVEKITTVESATEEKLTPVLAQKQAL 145

RESULT 4
ID Q7ZXY2 PRELIMINARY; PRT; 338 AA.
AC Q7ZXY2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Dcn2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Kozminski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.D., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RC Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC044069; AAH44069.1; -
DR GO: GO:0005869; C:dynactin complex; IEA.
DR GO: GO:0007017; P:microtubule-based process; IEA.
DR InterPro: IPR006996; Dnactin.
DR Pfam: PF04912; Dnactin; 1.
SQ SEQUENCE 338 AA; 38257 MW; 3346E0F0F644B186 CRC64;

Query Match 82.6%; Score 114; DB 2; Length 338;
Best Local Similarity 80.0%; Pred. No. 2e-06;
Matches 24; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVEKITTVESATEEKLTPVLAQKQAL 30
DB 51 EVEKITTVESATEEKLTPVLAQKQAL 80

RESULT 5
ID Q6IRB3 PRELIMINARY; PRT; 403 AA.
AC Q6IRB3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Dcn2-prov protein.
GN Name=Dcn2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hejbl F.,
RA Ditchenko L., Martina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stacieleto M., Soares M.B., Bonaldi A.F., Cavaletto T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holak S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
RA Blakesley R.W., Touchman T.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravynski M.I., Sklarska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 223:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070987; AAH70987.1; -.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
SQ SEQUENCE 403 AA; 44828 MW; 9PDI56C7C7983062 CRC64;

Query Match 82.6% Score 114; DB 2; Length 403;
Best Local Similarity 80.0%; Pred. No. 2.3e-06;
Matches 24; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVEKIKTTKVSATREKLTPTVILAKQAL 30
DB 116 EVEKIQSTLKESATEKLTPTVILAKQVAL 145

RESULT 6
ID Q66J30 PRELIMINARY; PRT; 403 AA.
AC Q66J30;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE MG82128 Protein.
GN Name=MG82128;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

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RT      initiative";
RN      Dev. Dyn. 225:384-391 (2002).
RN      [12]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Butlow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale P.,
RA      Hopkinso L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.C.,
RA      Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA      Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyzanski M.I., Skalska U., Smallue D.E., Schermer A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [13]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Klein S., Gerhard D.S.;
RL      Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.
DR      EMBL, BC081081; AAH81081.1; -
DR      InterPro: IPR006996; DnaMittin.
DR      Pfam: PF04912; DnaMittin; 1.
SQ      SEQUENCE 403 AA; 44737 MW; 86BBGCEB54325E93 CRC64;

Query Match          79.0%; Score 109; DB 2; Length 403;
Best Local Similarity 76.7%; Pred. No. 1e-05;
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

CY      1 EVEKITTVESATEEKLTPTVLAKKOLAAL 30
Db         116 EVETQSTVESAAAEKLTPTVALKOVASL 145

RESULT 7
OTTHH1 PRELIMINARY; PRT; 405 AA.
AC Q7T3H1.
DT 01-OCT-2003 (TREMBLrel. 25; Created)
DT 01-OCT-2003 (TREMBLrel. 25; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE Similar to dynactin 2 (P50).
GN ORFNames=zgc:63867;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Butlow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale P.,
RA      Hopkinso L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.C.,
RA      Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA      Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyzanski M.I., Skalska U., Smallue D.E., Schermer A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [13]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Klein S., Gerhard D.S.;
RL      Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.
DR      EMBL, BC081081; AAH81081.1; -
DR      InterPro: IPR006996; DnaMittin.
DR      Pfam: PF04912; DnaMittin; 1.
SQ      SEQUENCE 403 AA; 44737 MW; 86BBGCEB54325E93 CRC64;
```


RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravinsky M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053120; AAH53120.1; -;
 DR ZFIN; ZDB-GENE-040426-1279; zgc:63867.
 DR GO; GO:0005869; C:dynactin complex; IEA.
 DR GO; GO:0007017; P:microtubule-based process; IEA.
 DR InterPro; IPR006996; Dynactin.
 DR Pfam; Pf04912; Dynactin; 1.
 SQ SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;

Query Match 66.7%; Score 92; DB 2; Length 405;
 Best Local Similarity 63.3%; Pred. No. 0.0016;
 Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EVEKIKTVKESATEEKLTPVLAQKQAL 30
 Db 118 DVEKIQSTKESGAERLTPVLAQQAQL 147

RESULT 8

Q9PTG6 PRELIMINARY; PRT; 402 AA.
 ID Q9PTG6;
 AC Q9PTG6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Dynactin.
 GN Name=D50;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20056093; PubMed=10588646;
 RA Valetti C., Weizel D.M., Schrader M., Hasbani M.J., Gill S.R.,
 RA Kreis T.B., Schroer T.A.;
 RT "Role of dynactin in endocytic traffic: effects of dynactin
 RT overexpression and colocalization with CLIP-170.";
 RL Mol. Biol. Cell 10:4107-4120 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schroer T.A., Gill S.R., Hasbani J., Crego C.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF200744; AAF1396.1; -;
 DR GO; GO:0005869; C:dynactin complex; IEA.
 DR GO; GO:0007017; P:microtubule-based process; IEA.
 DR InterPro; IPR006996; Dynactin.
 DR Pfam; Pf04912; Dynactin; 1.
 SQ SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;

Query Match 64.5%; Score 89; DB 2; Length 402;
 Best Local Similarity 60.0%; Pred. No. 0.0039;
 Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVEKIKTVKESATEEKLTPVLAQKQAL 30
 Db 118 DVEKIQSTKESGAERLTPVLAQQAQL 147

RESULT 9

Q874E7 PRELIMINARY; PRT; 333 AA.
 ID Q874E7;
 AC Q874E7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MAT1-1-2.
 GN Name=MAT1-1-2;
 OS Paecilomyces tenuipes.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
 OX NCBI_TaxID=45847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15321663; DOI=10.1016/j.femsle.2004.06.033;
 RA Yokoyama E., Yamagishi K., Hara A.;
 RT "Development of a PCR-based mating-type assay for Clavicipitaceae.";
 RL FEMS Microbiol. Lett. 237:205-212 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22783895; PubMed=12902305;
 RX DOI=10.1128/AEM.69.8.5019-5022.2003;
 RA Yokoyama E., Yamagishi K., Hara A.;
 RT "Structures of the mating-type loci of Cordyceps takamontana.";
 RL Appl. Environ. Microbiol. 69:5019-5022 (2003).
 DR EMBL; AB096216; BAC67540.1; -;
 SQ SEQUENCE 333 AA; 37756 MW; 5590468907FEBBF6 CRC64;

Query Match 40.6%; Score 56; DB 2; Length 333;
 Best Local Similarity 44.8%; Pred. No. 59;
 Matches 13; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 VEKIKTVKESATEEKLTPVLAQKQAL 30
 Db 66 VNHIVDRIVERFSAEKIDPVLAQKQAL 94

RESULT 10

Q72JL4 PRELIMINARY; PRT; 445 AA.
 ID Q72JL4;
 AC Q72JL4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Biotin carboxylase (BC 6.3.4.14).
 GN OrderedlocustNames=TTCC0758;
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A., Brueggemann H., Raasch C., Wietzer A., Hartech T.,
 RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
 RA Jacobi C., Starkuviene V., Schlenceczek S., Dencker S., Huber R.,
 RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 RT thermophilus.";
 RL Nat. Biotechnol. 22:547-553 (2004).
 DR EMBL; AE017303; AAS81104.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004075; F:biotin carboxylase activity; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR004549; ACCC.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR005479; Cphg_synth_L_D2.
 DR InterPro; IPR011054; Rudmt_hyb_motif.
 DR Pfam; Pf02785; Biotin_carb_C; 1.

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DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR TIGRFAMs; TIGR00514; accC; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR Complete proteome.
SQ SEQUENCE 445 AA; 49302 MW; B57F7C8E914481A5 CRC64;

Query March 39.1%; Score 54; DB 2; Length 445;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 12; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Cy 5 IKTVKESATEBKLTPLVLAQ 26
    ||| ||| ||| ||| |||
Db 25 IKTVVASTADEKSLPVLAD 46

RESULT 11
ID C72Y ARATH STANDARD; PRT; 500 AA.
AC 09LIP3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cytochrome P450 71B37 (BC 1.14.-.-).
GN Name=CYP71B37; OrderedLocustNames=At3g26330; ORFNames=F20C19.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneo T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
RT and BAC clones."
RL DNA Res. 7:217-221(2000).
RN [2]
RP CONCEPTUAL TRANSLATION.
RP Bak S., Paquette S.;
RL Unpublished observations (APR-2001).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AP001298; BAB02193.1; ALT_SRQ.
DR HSSP; P00179; 1DT6.
DR GeneFarm; 1244; 94.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Heme; Monooxygenase; Multigene family; Oxidoreductase; Transmembrane.
FT TRANSMM 2 22 Iron (heme axial ligand) potential.
FT METAL 440 440 Iron (heme axial ligand) (By similarity).
SQ SEQUENCE 500 AA; 56843 MW; B36088363D918FE1 CRC64;

Query Match 39.1%; Score 54; DB 1; Length 500;
Best Local Similarity 43.3%; Pred. No. 1.6e+02;
Matches 13; Conservative 9; Mismatches 6; Indels 2; Gaps 1;
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Oy 1 EVEKITVKSATEBKLTPLVLAQ 30
    ||| ||| ||| ||| |||
Db 150 EVKTLNMFESAAQK--TEVNLSKSL 177

RESULT 12
ID 06BPD3 PRELIMINARY; PRT; 769 AA.
AC 06BPD3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hanseni chromosome E of strain CBS767 of Debaryomyces
DE hanseni.
GN ORFNames=DEHNOE150929;
OS Debaryomyces hanseni CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul I., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Cattelico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Falthed C., Ferry-Dumazet H., Groppi A.,
RA Hantreaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikoleki M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekaya F., Wesolowski-Jouvel M., Westhof E., Wirth B.,
RA Zeulou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Boulcher C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382137; CAG8181.1; -.
DR GO; GO:0005525; P:GTP binding; IEA.
DR GO; GO:0003746; P:translation elongation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_TII_V.
DR InterPro; IPR00517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; Protsyn_GTPbind.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF00764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF01144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATINFCT.
DR TIGRFAMs; TIGR00484; EF-G; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR GTP-binding; Protein biosynthesis.
SQ SEQUENCE 769 AA; 85013 MW; CA2EBCF3A8EBCC CRC64;

Query Match 39.1%; Score 54; DB 2; Length 769;
Best Local Similarity 37.0%; Pred. No. 2.4e+02;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
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Db          311 VEIKAAIRRAITARRFTPLVMSALA 337

RESULT 13
GLND_AZOB
ID GLND_AZOB STANDARD; PRT; 933 AA.
AC QOROD;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE [Protein-PII] uridylyltransferase (EC 2.7.7.59) (PII uridylyl-
DE transferase) (Uridylyl removing enzyme) (Urase).
GN Name=glnd;
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Azospirillum.
OX NCBI_TaxID=192;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Sp7 / ATCC 29145;
RA Van Dommelen A., Keijfers V., Somers E., Vanderleyden J.;
RT "Cloning and characterization of the Azospirillum brasilense glnd gene
RT and analysis of a glnd mutant.";
RL Mol. Genet. 265:813-820(2002).
CC -1- FUNCTION: Modifies, by uridylylation or deuridylylation the PII
CC (glnd) regulatory protein.
CC -1- CATALYTIC ACTIVITY: UTP + [protein-PII] = diphosphate + uridylyl-
CC [protein-PII].
CC -1- SIMILARITY: Belongs to the glnd family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: AF149716; AAL87737.1; -.
DR HAMAP: MF_00277; -.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR006674; HD_hydro.
DR InterPro: IPR003607; Met_Phos_hydro.
DR InterPro: IPR002934; NTP_transf.
DR InterPro: IPR010043; Urase_glnd.
DR Pfam: PF01842; ACT; 2.
DR Pfam: PF01966; HD; 1.
DR Pfam: PF01909; NTP_transf_2; 1.
DR SMART: SMO0471; HD; 1.
DR TIGRFAMs: TIGR01693; Urase_glnd; 1.
KW Nitrogen fixation; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 933 AA; 104601 MW; 35E692E0411BB9E7 CRC64;

Query Match          39.1%; Score 54; DB 1; Length 933;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Db          36 EDELTVAHGRTGDKPALIARLQAL 63

RESULT 14
ID Q6BF22 PRELIMINARY; PRT; 416 AA.
AC Q6BF22;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
DE ORFNames=PTMB_230;
GN Parametium tetraurelia.
OS

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OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Parametium.
OX NCBI_TaxID=5688;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RX PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
RA Zagulski M., Nowak J.K., De Mouel A., Nowacki M., Migdalski A.,
RA Gromadka R., Noel B., Blanc I., Dessen P., Winkler P., Keller A.M.,
RA Cohen J., Meyer E., Sperling L.;
RT "High Coding Density on the Largest Parametium tetraurelia Somatic
RT Chromosome.";
RL Curr. Biol. 14:1397-1404(2004).
RN
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RT "Parametium megabase sequencing project.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: CR348612; CAH03428.1; -.
DR InterPro: IPR001251; CRAL_TRIO_C.
DR PROSITE: PS50191; CRAL_TRIO; 1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 48774 MW; 883270A4B29101D1 CRC64;

Query Match          38.4%; Score 53; DB 2; Length 416;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Db          42 IEKIKTKKENGIDIKRSTILMLMA 69

RESULT 15
ID Q6CF32 PRELIMINARY; PRT; 710 AA.
AC Q6CF32;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similarity (Fragment).
GN ORFNames=YAL10B10692g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolévures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleyaeren C.,
RA Boisserie A., Boyer J., Cattivello L., Confarlier F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolaki M., Oztes S., Ozier-Kalogeropoulos O.,
RA Pellene S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolocin-Fukuhara M., Thierry A.,
RA Bouchler C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: CR382128; CAG82975.1; -.

```

DR InterPro; IPR005011; SART_1.
 DR Pfam; PF03343; SART-1; 1.
 FT NON TRR 1

SO SEQUENCE 710 AA; 81568 MW; 89C3CA466BB2F69B CRC64;

Query Match 38.4%; Score 53; DB 2; Length 710;
 Best local similarity 50.0%; Pred. No. 2.9e+02;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 6 KTYVKSATTEKLTTPVLLAKQLAA 29
 Db 426 KNLMKSQRRRKLTPEQLAEQLAA 449

Search completed: November 3, 2005, 22:03:01
 Job time : 55.7808 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:32:33 ; Search time 71.1872 Seconds
(without alignments)
282.516 Million cell updates/sec

Title: 09782816-51

Sequence: 1 GVKETPQOKTQRLHEVQEL.....ESATEEKLTPLYAKQLAAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:*
2: geneseqp19808:*
3: geneseqp2000s:*
4: geneseqp2000s:*
5: geneseqp2000s:*
6: geneseqp2000s:*
7: geneseqp2000s:*
8: geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251	100.0	314	ABM81421	Abm81421 Tumour-as
2	251	100.0	378	ABP98851	ABP98851 Human str
3	251	100.0	401	ADJ69563	ADJ69563 Human hea
4	251	100.0	406	ABP53018	ABP53018 Human p50
5	251	100.0	465	ABBS868	ABBS868 Breast an
6	248	98.8	183	ABP53019	ABP53019 Mouse p50
7	246	98.0	52	ABP53016	ABP53016 Cellular
8	231	92.0	134	AAG75956	AAg75956 Human col
9	113	45.0	22	ABP52968	ABP52968 Cellular
10	107	42.6	21	ABP52969	ABP52969 Cellular
11	103	41.0	20	ABP52970	ABP52970 Cellular
12	103	41.0	23	ABP52966	ABP52966 Cellular
13	98	39.0	19	ABP52971	ABP52971 Cellular
14	93	37.1	18	ABP52972	ABP52972 Cellular
15	88	35.1	17	ABP52973	ABP52973 Cellular
16	81	32.3	16	ABP52974	ABP52974 Cellular
17	76	30.3	15	ABP52975	ABP52975 Cellular
18	72.5	28.9	53	ABP53017	ABP53017 Cellular
19	72.5	28.9	380	ABBS988	ABBS988 Drosophi
20	72.5	28.9	380	ABP53020	ABP53020 Drosophi
21	71	28.3	14	ABP52976	ABP52976 Cellular
22	70	27.9	1087	ABBS5359	ABBS5359 Drosophi
23	70	27.9	1087	ABBS5358	ABBS5358 Drosophi
24	68	27.1	2368	AAU34139	AAU34139 Staphyloc
25	68	27.1	2368	AAU36796	AAU36796 Staphyloc

26	67	26.7	1448	6	ADA89551	Staphyloc
27	67	26.7	2478	4	AAU37374	Staphyloc
28	67	26.7	2478	4	AAU34320	Staphyloc
29	67	26.7	2478	6	ABJ19002	Pathogen
30	67	26.7	2478	6	ABM71899	Staphyloc
31	67	26.7	2481	6	ABU15838	Protein e
32	67	26.7	2481	7	ABR62804	Methicillin
33	66	26.3	13	5	ABP52977	ABP52977 Cellular
34	66	26.3	386	2	ABU44043	Protein e
35	66	26.3	868	2	AAV37731	Protein i
36	66	26.3	1020	4	AAW79875	Human pro
37	65.5	26.1	207	4	ABR29754	Human pro
38	65.5	26.1	1837	8	ADS4304	Rice pnt-
39	64	25.5	140	4	AAO12168	Bacterial
40	64	25.5	151	3	AAO37325	Human pol
41	64	25.5	188	2	AAW64545	Human sec
42	64	25.5	188	3	AAI10278	Human sec
43	64	25.5	188	4	AAU12172	Human fet
44	64	25.5	188	6	ABO17616	Human PRO
45	64	25.5	188	6	ABU80870	Novel hum

ALIGNMENTS

RESULT 1
ABM81421
ID ABM81421 standard; protein; 314 AA.

XX AC ABM81421;
XX DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.

XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX KW tumour; diagnosis; cell proliferative disorder; breast cancer;
XX KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX KW central nervous system cancer; bladder cancer; pancreatic cancer;
XX KW cervical cancer; melanoma; leukaemia; hybridisation probe;
XX KW chromosome identification; chromosome mapping; gene mapping;
XX KW gene therapy; cytostatic.

XX OS Homo sapiens.

XX PN MO2004030615-A2.

XX PD 15-APR-2004.

XX PE 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX PA (GETH) GENENTECH INC.

XX PI Wu TD, Zhang Z, Zhou Y;

XX DR WPI: 2004-347921/32.

XX N-PSDB: ACN39497.

XX PT New tumor-associated antigenic target polypeptides and nucleic acids,
XX PT useful in preparing a medicament for treating or detecting a
XX PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX PT prostate cancer or tumor.

XX PS Claim 12; SEQ ID NO 3675; 7273bp; English.

XX CC The invention relates to human tumour-associated antigenic target (TAT)
XX CC polypeptides, and their related nucleic acids. The TAT polypeptides are
XX CC overexpressed in cancer tissues compared to normal tissues, and may thus
XX CC serve as effective targets for the diagnosis and treatment of cancer in
XX CC mammals. The invention also relates to nucleic acid and polypeptide
XX CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAR nucleic acid; an antibody specific for a TAR polypeptide; a peptide or organic molecule which binds to a TAR polypeptide; fusion proteins comprising a TAR polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAR polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAR expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAR nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAR polypeptide of the invention

SO Sequence 314 AA;

Query Match 100.0%; Score 251; DB 8; Length 314;
Best Local Similarity 100.0%; Pred. No. 6e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKEPPOOKYQRLHEVOELTTEVEKIKTYKESATEBKLPVLLAQAL 52
Db 7 GVKEPPOOKYQRLHEVOELTTEVEKIKTYKESATEBKLPVLLAQAL 58

RESULT 2
ABP98851 ID ABP98851 standard; protein; 378 AA.
XX AC ABP98851;
XX DT 15-JUN-2003 (first entry)
XX DE Human structural and cytoskeletal associated protein #42.
XX KW Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal; neuroprotective; cerebroprotective; hypotensive; cardiast; osteoplastic; antiinflammatory; antiarthritic; vinicide; gene therapy; human; stroke; structural and cytoskeleton-associated protein; SCAP; cancer; angina; atherosclerosis; epilepsy; Huntington's disease; hypertension; heart failure; osteoporosis; osteoarthritis.
XX KM
XX OS Homo sapiens.
XX PN WO2003031940-A2.
XX PD 17-APR-2003.
XX PF 10-OCT-2002; 2002WO-US032851.
XX PR 12-OCT-2001; 2001US-0328931P.
PR 19-OCT-2001; 2001US-0360681P.
PR 02-NOV-2001; 2001US-0343896P.
PR 09-NOV-2001; 2001US-0346308P.
PR 16-NOV-2001; 2001US-0332385P.
PR 07-DEC-2001; 2001US-0340776P.
PR 11-JAN-2002; 2002US-0347703P.
XX PA (INCYTE) GENOMICS INC.
XX PI Becha SD, Bhacia U, Blake JF, Borowsky ML, Burrill JD, Chang H, Chawla NK, Elliott VS, Emerling BM, Forsythe JF, Goryad AE, Lal PG, Griffin JA, Hafalia AD, Ho A, Ison CH, Kabie AE, Khare R, Lal PG, Lee S, Lee BA, Lee SY, Lehr-Mason PM, Li JX, Lindquist EA, Luo W, Marquis JP, Ramkumar J, Richardson TW, Sprague WM, Swarnakar A, Tang YF, Warren BA, Yang J, Yue H, Zebardjian Y, Zheng W;
XX WPI; 2003-403125/38.
XX DR N-PSDB; ACC44338.
XX PT New human structural and cytoskeleton-associated proteins (SCAP) useful for diagnosing, treating and preventing diseases or conditions associated

PT with the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
XX Claim 1; Page 298; 361pp; English.
XX CC This sequence represents a novel isolated human structural and cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and polynucleotides encoding them are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or over expression of SCAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), heart (e.g. hypertension, heart failure, angina) and skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles

SO Sequence 378 AA;

Query Match 100.0%; Score 251; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.4e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKEPPOOKYQRLHEVOELTTEVEKIKTYKESATEBKLPVLLAQAL 52
Db 71 GVKEPPOOKYQRLHEVOELTTEVEKIKTYKESATEBKLPVLLAQAL 122

RESULT 3
ADJ69563 ID ADJ69563 standard; protein; 401 AA.
XX AC ADJ69563;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SegID1369.
XX DE
XX KW mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytosstatic.
XX KM
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0369987P.
PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PI (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW, Warnock DE;
XX WPI; 2003-845369/78.
XX DR
XX PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.
XX
PS Claim 1; SEQ ID NO 1369; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiatherosclerotic, osteoprotective, ophthalmological and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 251; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 7,9e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAKQLAAL 52
DB 94 GVKETPOOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAKQLAAL 145
|||||
RESULT 4
ABP53018
ID ABP53018 standard; protein; 406 AA.
XX
AC ABP53018;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human p50 amino acid sequence SEQ ID NO:53.
XX
KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macropagal disorder; epithelial disorder;
KW stromal disorder; blastocoelec disorder; angiogenic disorder;
KW immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200264779-A2.
XX
PD 22-AUG-2002.
XX
PE 21-JAN-2002; 2002WO-US001708.
XX
PR 14-FEB-2001; 2001US-00782816.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Sharp DJ, Rogers GC, Scholey JM;
XX
DR WPI; 2002-657599/70.
XX
PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.
XX
PS Disclosure; Fig 1; 55pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (I) have cytoskeletal and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macropagal, epithelial, stromal and blastocoelec disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents human p50 which is given in the exemplification of the present
CC invention
XX
SQ Sequence 406 AA;

Query Match 100.0%; Score 251; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 8,1e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAKQLAAL 52
DB 99 GVKETPOOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAKQLAAL 150
|||||
RESULT 5
AAB58968
ID AAB58968 standard; protein; 465 AA.
XX
AC AAB58968;
XX
DT 27-MAR-2001 (first entry)
XX
DE Breast and ovarian cancer associated antigen protein sequence SRQ ID 676.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PE 08-MAR-2000; 2000WO-US005881.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/58.
XX
DR N-PSDB; AAF21871.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention, treatment
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 11; Page 1126-1128, 1299pp; English.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic, immunosuppressive, nocotropic;
CC neuroprotective; antiviral; antiallergic; hepatocytic; antidiabetic;
CC antiinflammatory; antitumor; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases

CC Sequence 465 AA;

Query Match 100.0%; Score 251; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 9,4e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKETPOOKYORLHVEQELTTEVEKIKTYKESATBEKLTPLVLAQQLAL 52
|||
Db 158 GVKETPOOKYORLHVEQELTTEVEKIKTYKESATBEKLTPLVLAQQLAL 209

RESULT 6
AAB53019 ID AAB53019 standard; protein; 183 AA.

XX AAB53019;

DT 05-NOV-2002 (first entry)

XX Mouse p50 amino acid sequence SEQ ID NO:54.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumor; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoeleic disorder; angiogenic disorder;
KM immunologic disorder.

XX Mus musculus.

XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JM;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

XX Disclousure; Fig 2; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in AAB52966 and AAB52967 and can have C-terminal and N-
CC terminal extensions. (I) have cytostatic and antiinflammatory activities

CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents mouse p50 which is given in the exemplification of the present
CC invention

CC Sequence 183 AA;

Query Match 98.8%; Score 248; DB 5; Length 183;
Best Local Similarity 98.1%; Pred. No. 7,1e-21;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKETPOOKYORLHVEQELTTEVEKIKTYKESATBEKLTPLVLAQQLAL 52
|||
Db 94 GVKETPOOKYORLHVEQELTTEVEKIKTYKESATBEKLTPLVLAQQLAL 145

RESULT 7
AAB53016 ID AAB53016 standard; peptide; 52 AA.

XX AAB53016;

DT 05-NOV-2002 (first entry)

XX Cellular proliferation peptide inhibitor SEQ ID NO:51.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumor; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoeleic disorder; angiogenic disorder;
KM immunologic disorder.

XX Homo saplens.

XX Mus musculus.

XX Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 44 /label= 'Leu, Val
FT /note= "Leu in humans and Val in Mus musculus"

XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JM;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

XX Claim 2; Page 31; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoele disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a specifically claimed peptide inhibitor of cellular
CC proliferation from the present invention

XX
XX
SQ Sequence 52 AA;

Query Match 98.0%; Score 246; DB 5; Length 52;
Best Local Similarity 98.1%; Pred. No. 2.8e-21;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVKETPOOKYQRLHEVOELTTEVEKIKTYVESATEERKLPVLLAKQALAL 52
Db 1 GVKETPOOKYQRLHEVOELTTEVEKIKTYVESATEERKLPVLLAKQALAL 52

RESULT 8
AAG75956
ID AAG75956 standard; protein; 134 AA.
XX
XX AAG75956;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:6720.
XX
XX Human colon cancer antigen protein SEQ ID NO:6720.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 12.
XX
XX Homo sapiens.
XX
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US026524.
XX
XX 29-SEP-1999; 99US-0157137P.
XX 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX N-PSDB; AAH35361.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11; Page 8181; 9803pp; English.

XX
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used

CC to produce the colon cancer-associated Pe, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922

XX
XX
SQ Sequence 134 AA;

Query Match 92.0%; Score 231; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPQOKYQRLHEVOELTTEVEKIKTYVESATEERKLPVLLAKQALAL 52
Db 1 TPQOKYQRLHEVOELTTEVEKIKTYVESATEERKLPVLLAKQALAL 48

RESULT 9
ABP52968
ID ABP52968 standard; peptide; 22 AA.
XX
XX ABP52968;
XX
XX 05-NOV-2002 (first entry)
XX
XX Cellular proliferation inhibitor related peptide SEQ ID NO:3.
XX
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
XX sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
XX glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
XX glandular disorder; macrophagal disorder; epithelial disorder;
XX stromal disorder; blastocoele disorder; angiogenic disorder;
XX immunologic disorder.
XX
XX Homo sapiens.
XX Mus musculus.
XX Synthetic.
XX
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JW;
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Claim 1; Page 29; 55pp; English.

XX
XX
XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (1) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumours (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and

CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 22 AA;

Query Match 45.0%; Score 113; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYQRLHVEVQLTT 22
Db 1 GVKETPOOKYQRLHVEVQLTT 22

RESULT 10
ABP52969
ID ABP52969 standard; peptide; 21 AA.
XX
AC ABP52969;
XX
DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:4.
XX
DE Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.

XX Homo sapiens.
OS Mus musculus.
OS Synthetic.
OS
XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JM;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.

XX Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumours); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoeleic disorders; and

CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 21 AA;

Query Match 42.6%; Score 107; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKETPOOKYQRLHVEVQLTT 22
Db 1 VKETPOOKYQRLHVEVQLTT 21

RESULT 11
ABP52970
ID ABP52970 standard; peptide; 20 AA.
XX
AC ABP52970;
XX
DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:5.
XX
DE Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.

XX Homo sapiens.
OS Mus musculus.
OS Synthetic.
OS
XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JM;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.

XX Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumours); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoeleic disorders; and
XX represents a peptide that can be N-terminally added to (P1)

SQ Sequence 20 AA;
Query Match 41.0%; Score 103; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 KETPOQKRYRLHVEQELTT 22
1 KETPOQKRYRLHVEQELTT 20
DB
RESULT 12
ABP52966
ID ABP52966 standard; peptide; 23 AA.
AC ABP52966;
DT 05-NOV-2002 (first entry)
XX Cellular proliferation inhibitor related peptide SEQ ID NO:1.
DE
XX Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeic disorder; angiogenic disorder;
KW immunologic disorder.
XX
XX Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 22 /label= 'Leu, Val
FT /note= "Leu in humans and Val in Mus musculus"
XX
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer: by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Claim 1; Page 29; 55pp; English.
XX
XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumours (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumours); leukaemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoeic disorders; and
XX inflammatory, angiogenic and immunologic disorders

XX
SQ Sequence 23 AA;
Query Match 41.0%; Score 103; DB 5; Length 23;
Best Local Similarity 95.7%; Pred. No. 5.3e-05;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 23 EWEKIKTTVKESATEBKLPVLL 45
1 EWEKIKTTVKESATEBKLPVXL 23
DB
RESULT 13
ABP52971
ID ABP52971 standard; peptide; 19 AA.
AC ABP52971;
DT 05-NOV-2002 (first entry)
XX Cellular proliferation inhibitor related peptide SEQ ID NO:6.
DE
XX Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeic disorder; angiogenic disorder;
KW immunologic disorder.
XX
XX Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Claim 1; Page 29; 55pp; English.
XX
XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumours (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoeic disorders; and
XX inflammatory, angiogenic and immunologic disorders. The present sequence
XX represents a peptide that can be N-terminally added to (P1)
SQ Sequence 19 AA;

Query Match 39.0%; Score 98; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ETPOOKYORLHVEVQLTT 22
Db 1 ETPOOKYORLHVEVQLTT 19

RESULT 14

ABP52972 ID ABP52972 standard; peptide; 18 AA.

AC ABP52972;

DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:7.

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastococelic disorder; angiogenic disorder;
KW immunologic disorder.

OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

PN WO200264779-A2.

PD 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

PI Sharp DJ, Rogers GC, Scholey JM;

DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

PS Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumors); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastococelic disorders; and
XX inflammatory, angiogenic and immunologic disorders. The present sequence
XX represents a peptide that can be N-terminally added to (P1)

XX Sequence 18 AA;

Query Match 37.1%; Score 93; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TPPOOKYORLHVEVQLTT 22
Db 1 TPPOOKYORLHVEVQLTT 18

RESULT 15

ABP52973 ID ABP52973 standard; peptide; 17 AA.

AC ABP52973;

DT 05-NOV-2002 (first entry)

XX Cellular proliferation inhibitor related peptide SEQ ID NO:8.

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastococelic disorder; angiogenic disorder;
KW immunologic disorder.

OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

PN WO200264779-A2.

PD 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

PI Sharp DJ, Rogers GC, Scholey JM;

DR WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

PS Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumors); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastococelic disorders; and
XX inflammatory, angiogenic and immunologic disorders. The present sequence
XX represents a peptide that can be N-terminally added to (P1)

XX Sequence 17 AA;

Query Match 35.1%; Score 88; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 POKKORLHEVELETT 17

Search completed: November 3, 2005, 21:57:30
Job time : 72.1872 secs

01:21:40:00 00:00:00

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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:32:33 ; Search time 41.0695 Seconds
(without alignments)
282.516 Million cell updates/sec

Title: 09782816-1-22

Sequence: 1 EVEKIKTTVKESATBEKLTPTVLAKQLAAL 30 $\chi_1 = 0$

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 $(\chi_1) \delta S_{eq}(D)$

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp19808.*
2: Geneseqp19908.*
3: Geneseqp20008.*
4: Geneseqp20018.*
5: Geneseqp20028.*
6: Geneseqp20038.*
7: Geneseqp20048.*
8: Geneseqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	138	100.0	134	AAg75956 Human col
2	138	100.0	314	ABM81421 Tumour-as
3	138	100.0	378	ABP98851 Human str
4	138	100.0	401	ADJ69563 Human hea
5	138	100.0	406	ABP53018 Human p50
6	138	100.0	465	AAH58968 Breast an
7	138	97.8	183	ABP53019 Mouse p50
8	133	96.4	52	ABP53016 Cellular
9	103	74.6	23	ABP52966 Cellular
10	56	40.6	334	ADH10326 Allicococ
11	51	37.0	932	ABU19329 Protein e
12	51	37.0	10917	AAE36132 Streptom
13	50	36.2	210	AAAG61007 Arabidops
14	50	36.2	210	AAAG17748 Arabidops
15	50	36.2	640	ABU16767 Protein e
16	50	36.2	773	AAU35737 Helicobac
17	50	36.2	773	ABU30798 Protein e
18	50	36.2	855	AAU99662 Human his
19	50	36.2	855	ADC21699 Human his
20	50	36.2	855	ADH96563 Human his
21	50	36.2	912	ADH43346 Human cla
22	50	36.2	915	ABP56824 Human his
23	50	36.2	933	ABM85826 Mouse pro
24	50	36.2	938	ADJ77693 Murine hi
25	50	36.2	1008	AAH78891 Human pro

26	50	36.2	1020	4	AAH79875 Human pro
27	50	36.2	1642	8	ADQ39513 Human myo
28	50	36.2	1642	8	ADQ39515 Human myo
29	50	36.2	2000	8	ADN04531 Antipsoe-i
30	50	36.2	2000	8	ADP23738 PRO polyP
31	50	36.2	3024	7	ADJ70171 Human hea
32	50	36.2	3396	7	ADD48597 Human pro
33	50	36.2	3396	7	ADN95526 Human BEC
34	50	36.2	3396	8	ADJ75521 Marker ge
35	50	36.2	3396	8	ADQ39509 Human myo
36	50	36.2	3396	8	ADQ39510 Human myo
37	50	36.2	3396	8	ADP99164 Chondroci
38	49	35.5	87	4	ABR38983 Peptide #
39	49	35.5	87	4	AAH32468 Peptide #
40	49	35.5	87	4	AAH72208 Human Don
41	49	35.5	87	4	AAH59635 Human bra
42	49	35.5	87	4	ABG53895 Human liv
43	49	35.5	87	5	ABG42023 Human pep
44	49	35.5	279	6	ABU29933 Protein e
45	49	35.5	340	8	ADQ19111 Human sol

ALIGNMENTS

RESULT 1
AAH75956
ID AAG75956 standard; protein; 134 AA.

XX
AC AAG75956;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6720.
XX
KM Human, colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 12.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
PD
PD 05-APR-2001.
PF
PF 28-SEP-2000; 2000WO-US026524.
PR
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI, 2001-235357/24.
XX N-PSDB; AAH35361.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11, Page 8181; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used
XX to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P

CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
CC
XX
SQ Sequence 134 AA;
Query Match 100.0%; Score 138; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EVEKIKTVKESATEBKLTPLYLAKQAL 30
Db 19 EVEKIKTVKESATEBKLTPLYLAKQAL 48
RESULT 2
ABM81421
ID ABM81421 standard; protein; 314 AA.
XX
AC ABM81421;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
FN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN39497.
XX
PT New tumour-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3675; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with

CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 314 AA;
Query Match 100.0%; Score 138; DB 8; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EVEKIKTVKESATEBKLTPLYLAKQAL 30
Db 29 EVEKIKTVKESATEBKLTPLYLAKQAL 58
RESULT 3
ABP98851
ID ABP98851 standard; protein; 378 AA.
XX
AC ABP98851;
XX
DT 15-JUL-2003 (first entry)
XX
DE Human structural and cytoskeletal associated protein #42.
XX
KW Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal;
KW neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic;
KW antiinflammatory; antiarthritic; virocidic; gene therapy; human; stroke;
KW structural and cytoskeleton-associated protein; SCAP; cancer; angina;
KW atherosclerosis; epilepsy; Huntington's disease; hypertension;
KW heart failure; osteoporosis; osteoarthritis.
XX
OS Homo sapiens.
XX
FN WO2003031940-A2.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-US032851.
XX
PR 12-OCT-2001; 2001US-0328931P.
PR 19-OCT-2001; 2001US-0360641P.
PR 02-NOV-2001; 2001US-0343886P.
PR 09-NOV-2001; 2001US-0346308P.
PR 16-NOV-2001; 2001US-0332385P.
PR 07-DEC-2001; 2001US-0340776P.
PR 11-JAN-2002; 2002US-0347703P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Becha SD, Bhatia U, Blake JF, Borowsky ML, Burrill JD, Chang H,
XX
PI Chawla NK, Elliott VS, Emerling BM, Forsythe JD, Goryad AE,
PI Griffin JA, Hafalia AYA, Ho A, Ison CH, Kable AE, Khare R, Lal PG,
PI Lee S, Lee EA, Lee SY, Lehr-Mason PM, Li JX, Lindquist EA, Luo W,
PI Marquis JP, Rankumar J, Richardson TW, Sprague WW, Swarnakar A,
PI Tang YT, Warren BA, Yang J, Yue H, Zebardjian Y, Zheng W;
XX
DR WPI; 2003-403125/38.
DR N-PSDB; ACC44338.
XX
PT New human structural and cytoskeleton-associated proteins (SCAP) useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
XX
PS Claim 1; Page 298; 361pp; English.
XX
CC This sequence represents a novel isolated human structural and
CC cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and
CC polynucleotides encoding them are useful in diagnosing, treating and

CC preventing diseases or conditions associated with the decreased
CC expression or over expression of SCAP, such as cell proliferative (e.g.
CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and
CC skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral
CC infections. These are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC SCAP. The SCAP or its fragments are useful in screening compounds for
CC effectiveness as agonist or antagonist of the polypeptides, or in
CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to or modulate the activity of the polypeptide. The
CC microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles

XX Sequence 378 AA;
SQ

Query Match 100.0%; Score 138; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 3,9e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVEKIKTTVESATBEKLTPLYLAKQIAL 30
Db 93 EVEKIKTTVESATBEKLTPLYLAKQIAL 122

RESULT 4
ADJ69563 standard; protein; 401 AA.
XX ADJ69563;
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1369.
XX
XX mtDNA; human; screening assay; diabetes mellitus;
KM Huntington's disease; osteoarthritis;
KM Leber's hereditary optic neuropathy; LHON;
KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KM neuroprotective; neurotrophic; antidiabetic; anticonvulsant; antiarthritic;
KM osteopathic; ophthalmological; cytostatic.

XX Homo sapiens.
OS
XX
XX WO2003087768-A2.
PN
XX
XX 23-OCT-2003.
PD
XX
XX 04-APR-2003; 2003WO-US010870.
PF
XX
XX 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.
DR
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

XX Claim 1; SEQ ID NO 1369; 180bp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotrophic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 401 AA;
SQ

Query Match 100.0%; Score 138; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVEKIKTTVESATBEKLTPLYLAKQIAL 30
Db 116 EVEKIKTTVESATBEKLTPLYLAKQIAL 145

RESULT 5
ABP53018 standard; protein; 406 AA.
XX ABP53018;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
DE Human p50 amino acid sequence SEQ ID NO:53.
XX
XX Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynamin inhibitor; gene therapy; tumour; carcinoma;
KM sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytic disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophegal disorder; epithelial disorder;
KM stromal disorder; blastocoeleic disorder; angiogenic disorder;
KM immunologic disorder.

XX Homo sapiens.
OS
XX
XX WO200264779-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 21-JAN-2002; 2002WO-US001708.
PF
XX
XX 14-FEB-2001; 2001US-00782816.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Sharp DJ, Rogers GC, Scholey JM;
PI WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynamin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

XX Disclosure; Fig 1; 55pp; English.
XX
XX The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (I) have cyostatic and antiinflammatory activities
CC and can be used as p50/dynamin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,

CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, malignantomas, and various 'head and
CC neck tumours'; leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macropagagal, epithelial, stromal and blascoeolic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents human p50 which is given in the exemplification of the present
XX invention

Sequence 406 AA;
SQ

Query Match	100.0%;	Score 138;	DB 5;	Length 406;
Best Local Similarity	100.0%;	Pred. No. 4.3e-11;		
Matches 30; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 EVEKIKTTVKESATEEKLTPVLLAKOLAAL 30
        |||||
Db     121 EVEKIKTTVKESATEEKLTPVLLAKOLAAL 150
```

RESULT 6

ID AAB58968 standard; protein; 465 AA.

AC AAB58968;

DT 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 676.

Human, breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KM neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KM antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
 KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KM Addison's disease; allergy; autoimmune haemolytic anaemia;
 KM autoimmune thyroiditis; diabetes mellitus; Croun's disease;
 KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KM cardiovascular disorder; wound healing; neurological disease.

Homo sapiens.

PN WO200055173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US005881.

PR 12-MAR-1999; 99US-0124270P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

WPI; 2000-611515/58.

X

PT polypeptides encoded by these genes, useful in the prevention, treatment

neurological diseases.

PS Claim 11; Page 1126-1128; 1299pp; English

CC Sequences AAF22614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterization of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive; nocotropic;
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC antiinflammatory; antileukemic; vulnerable; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and

CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and antagonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases

Query Match	100.0%	Score 138; DB 3;	Length 465;
Best Local Similarity	100.0%;	Pred. No. 5e-11;	
Matches 30; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

```
QY      1 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
          |||||
Db     180 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 209
```

RESULT 7

ID ABP53019 standard; protein; 183 AA.

AC ABP53019;

DT 05-NOV-2002 (first entry)

DE	Mouse p50 amino acid sequence	SEQ ID NO:54
DE		

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytic disorder; hypothalamic disorder; inflammatory;
KW glauclular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoele disorder; angiogenic disorder;
KW immunologic disorder.

Musculus.

AA WO200264779-A2.
PN

PD 22-AUG-2002.

21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

PA (REGC) UNIV CALIFORNIA.

Sharp DJ, Rogers GC, Scholey JM;

WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynaminin useful for treating cancer by

PT leukemia and lymphoid malignancies, or inflammatory and angiogenic and

XX
FI
XXXXXXXXXXXXX

The present invention describes an isolated (1) comprising or having at least 90% identity to (p1) or (p2) where (p1) and (p2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (1) have cytostatic and antiinflammatory activities and can be used as p50/dynactin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, cervical, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid malignancies, other disorders such

CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents mouse p50 which is given in the exemplification of the present
CC invention

XX Sequence 183 AA;

Query Match 97.8%; Score 135; DB 5; Length 183;
Best Local Similarity 96.7%; Pred. No. 4.5e-11;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EVEKIKTVKESATEEKLTPVLAKQAL 30
Db 116 EVEKIKTVKESATEEKLTPVLAKQAL 145

RESULT 8
ABP53016
ID ABP53016 standard; peptide; 52 AA.

XX ABP53016;
XX
XX
XX 05-NOV-2002 (first entry)

DE Cellular proliferation peptide inhibitor SEQ ID NO:51.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
XX sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
XX glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
XX glandular disorder; macrophagal disorder; epithelial disorder;
XX stromal disorder; blastocoeleic disorder; angiogenic disorder;
XX immunologic disorder.

XX Homo sapiens.
XX Mus musculus.
XX Synthetic.

XX Key Location/Qualifiers
XX Misc-difference 44
XX /label= 'Leu, Val
XX /note= "Leu in humans and Val in Mus musculus"

XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JW;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynamitin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.

XX Claim 2; Page 31; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynamitin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumours (renal, liver, kidney, bladder, breast,

CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a specifically claimed peptide inhibitor of cellular
CC proliferation from the present invention

XX Sequence 52 AA;

Query Match 96.4%; Score 133; DB 5; Length 52;
Best Local Similarity 96.7%; Pred. No. 2e-11;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 EVEKIKTVKESATEEKLTPVLAKQAL 30
Db 23 EVEKIKTVKESATEEKLTPVLAKQAL 52

RESULT 9
ABP52966
ID ABP52966 standard; peptide; 23 AA.

XX ABP52966;
XX
XX
XX 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:1.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
XX sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
XX glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
XX glandular disorder; macrophagal disorder; epithelial disorder;
XX stromal disorder; blastocoeleic disorder; angiogenic disorder;
XX immunologic disorder.

XX Homo sapiens.
XX Mus musculus.
XX Synthetic.

XX Key Location/Qualifiers
XX Misc-difference 22
XX /label= 'Leu, Val
XX /note= "Leu in humans and Val in Mus musculus"

XX WO200264779-A2.

XX 22-AUG-2002.

XX 21-JAN-2002; 2002WO-US001708.

XX 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.

XX Sharp DJ, Rogers GC, Scholey JW;

XX WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynamitin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.

XX Claim 1; Page 29; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (I) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynamitin inhibitors and in gene therapy. The

CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytic, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoele disorders; and
CC inflammatory, angiogenic and immunologic disorders
XX
SQ Sequence 23 AA;

Query Match 74.6%; Score 103; DB 5; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.5e-07;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEKIKTVKESATEKLTPLVL 23
DB 1 EVEKIKTVKESATEKLTPLVL 23

RESULT 10
ADBI0326

ID ADBI0326 standard; protein; 334 AA.

XX ADBI0326;

XX 20-NOV-2003 (first entry)

DE Alloiococcus otitis antigenic protein SEQ ID NO:4734.

XX Alloiococcus otitidis; antigenic protein; immunogenic; immunisation;
KW gene therapy; Gram-positive bacterium; infection.

XX Alloiococcus otitis.

OS WO2003048304-A2.

PN 12-JUN-2003.

PD 25-NOV-2002; 2002WO-US036123.

XX 29-NOV-2001; 2001US-0333777P.

PR 18-NOV-2002; 2002US-0426742P.

XX (AMHP) WYETH HOLDINGS CORP.

PA Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;

XX WPI; 2003-505284/47.

DR N-PSDB; ADBI0329.

XX New Alloiococcus otitidis polynucleotides and polypeptides, useful for
PT treating and diagnosing diseases, drug screening assays and monitoring of
PT effects during drug clinical trials.

XX Claim 33; SEQ ID NO 4734; 1019pp; English.

XX The present invention describes an isolated polynucleotide (1) of
CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
CC expression vector comprising the novel isolated polynucleotide (1), its
CC complement, degenerate variant or fragment; (3) a genetically engineered
CC host cell, transfected, transformed or infected with the vector of (2);
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
CC composition comprising the polypeptide, its complement, biological
CC equivalent or fragment, or the polynucleotide that is comprised in the
CC expression vector; (6) a pharmaceutical composition comprising the
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
CC of the polypeptides of (1), their biological equivalent or fragment; (8)
CC immunising against Alloiococcus otitidis by administering to a host the
CC immunogenic composition; (9) detecting and/or identifying Alloiococcus

CC otitidis in the biological sample; (10) a kit comprising a container
CC containing the novel polynucleotide, its degenerate variant or fragment,
CC or the antibody of (4); and (11) producing a polypeptide by culturing the
CC genetically engineered host cell under conditions suitable to produce the
CC polypeptide from the culture. (1) can be used in gene therapy. The
CC polynucleotides, polypeptides, antibodies and compositions of the present
CC invention can be used for treating and diagnosing diseases, drug
CC screening assays and monitoring of effects during drug clinical trials.
CC The polynucleotides are useful for expressing and detecting Alloiococcus
CC otitidis. The present sequence represents an Alloiococcus otitidis
CC antigen protein from the present invention.

XX Sequence 334 AA;

Query Match 40.6%; Score 56; DB 6; Length 334;
Best Local Similarity 34.5%; Pred. No. 17;
Matches 10; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 2 VEKIKTVKESATEKLTPLVLAKQLAAL 30
DB 244 IDQIKSTIKSGSVKTKLGGILIKKDLSSL 272

RESULT 11
ABU19329

ID ABU19329 standard; protein; 932 AA.

XX ABU19329;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #4856.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Borrelia burgdorferi.

OS WO200277183-A2.

PN 03-OCT-2002.

PD 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-023926/02.

DR N-PSDB; ACA23199.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 47253; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for

PR 18-MAY-1999;	99US-0134768P.
PR 19-MAY-1999;	99US-0134941P.
PR 20-MAY-1999;	99US-0135124P.
PR 21-MAY-1999;	99US-0135353P.
PR 24-MAY-1999;	99US-0135629P.
PR 25-MAY-1999;	99US-0136021P.
PR 27-MAY-1999;	99US-0136392P.
PR 28-MAY-1999;	99US-0136782P.
PR 01-JUN-1999;	99US-0137222P.
PR 03-JUN-1999;	99US-0137528P.
PR 04-JUN-1999;	99US-0137502P.
PR 07-JUN-1999;	99US-0137724P.
PR 08-JUN-1999;	99US-0138094P.
PR 10-JUN-1999;	99US-0138540P.
PR 10-JUN-1999;	99US-0138847P.
PR 14-JUN-1999;	99US-0139119P.
PR 16-JUN-1999;	99US-0139452P.
PR 16-JUN-1999;	99US-0139453P.
PR 17-JUN-1999;	99US-0139492P.
PR 18-JUN-1999;	99US-0139454P.
PR 18-JUN-1999;	99US-0139455P.
PR 18-JUN-1999;	99US-0139457P.
PR 18-JUN-1999;	99US-0139458P.
PR 18-JUN-1999;	99US-0139459P.
PR 18-JUN-1999;	99US-0139460P.
PR 18-JUN-1999;	99US-0139461P.
PR 18-JUN-1999;	99US-0139462P.
PR 18-JUN-1999;	99US-0139463P.
PR 18-JUN-1999;	99US-0139750P.
PR 21-JUN-1999;	99US-0139763P.
PR 22-JUN-1999;	99US-0139817P.
PR 23-JUN-1999;	99US-0139899P.
PR 23-JUN-1999;	99US-0140353P.
PR 23-JUN-1999;	99US-0140354P.
PR 24-JUN-1999;	99US-0140695P.
PR 28-JUN-1999;	99US-0140823P.
PR 29-JUN-1999;	99US-0140991P.
PR 30-JUN-1999;	99US-0141287P.
PR 01-JUL-1999;	99US-0141842P.
PR 01-JUL-1999;	99US-0142154P.
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Best Local Similarity 50.0%; Pred. No. 71;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Cy 1 EVEKIKTVKESATREKL 18
Db 174 EPERVKTWIEEFLTEKTI 191

RESULT 14
AA017748
ID AA017748 standard; protein; 210 AA.
XX
AC AA017748;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18886.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
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	Best Local Similarity	50.0%;	Pred. No.	71;	
	Matches 9; Conservative	5;	Mismatches	4;	Indels 0; Gaps 0
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ID	ABU16767 standard; protein; 640 AA.				
XX AC	ABU16767;				
DT	19-JUN-2003 (first entry)				
DE	Protein encoded by Prokaryotic essential gene #2294.				
XX XX	An antisense; prokaryotic essential gene; cell proliferation; drug design. Acinetobacter baumannii. WO200277183-A2. 03-OCT.-2002. 21-MAR-2002; 2002MO-US009107. PF PF PR 21-MAR-2001; 2001US-00815242; PR 06-SEP-2001; 2001US-00948993; PR 25-OCT-2001; 2001US-0342923P. PR 08-FEB-2002; 2002US-00072851. PR 06-MAR-2002; 2002US-0362699P. XA PA (ELIT-) ELITRA PHARM INC. Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW, PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; DR WPI; 2003-029926/02. N-PsDB; ACA20637.				
PT PT	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.				
PS PS	Claim 25; SEQ ID NO 44691; 1766pp; English.				
CC CC	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (?) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-regulated gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required				

CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 640 AA;

Query Match 36.2%; Score 50; DB 6; Length 640;
 Best Local Similarity 39.3%; Pred. No. 2.6e+02;
 Matches 11; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 3 EKIKTVESATBEKLTPTVLAKQIALAL 30
 : : ||| : : : : : : : : : :
 Db 131 DKYQKLVKESKASDEITQHLMLPMLRAL 158

Search completed: November 3, 2005, 21:57:27
 Job time : 44.0695 secs

09782816-1-22.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 10.9091 Seconds
(without alignments)
264.596 Million cell updates/sec

Title: 09782816-1-22

Perfect score: 138

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	38.4	1394	2 T34061	hypothetical prote
2	51	37.0	773	2 B71931	DNA gyrase chain B
3	51	37.0	932	2 C70191	penicillin-binding
4	50.5	36.6	191	2 AF0580	lipoate-protein li
5	50	36.2	210	2 B64499	hypothetical prote
6	50	36.2	773	2 B64582	DNA gyrase, sub B
7	50	36.2	878	2 T17245	hypothetical prote
8	50	36.2	1151	2 AG1717	probable peptidog
9	49	35.5	298	2 B82707	carboxyphosphoen
10	49	35.5	340	2 T42684	hypothetical prote
11	49	35.5	455	2 B71480	hypothetical prote
12	48.5	35.1	311	1 IQBS44	probable agx-1 hom
13	48.5	34.8	211	2 T52431	primosome compon
14	48	34.8	379	2 T34100	hypothetical prote
15	48	34.8	1112	2 D75056	hypothetical prote
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17	48	34.8	2515	2 A41519	hypothetical prote
18	47.5	34.4	225	2 E84423	posterior-group pr
19	47	34.1	103	2 T07234	hypothetical prote
20	47	34.1	138	2 AD1154	ribosomal protein
21	47	34.1	138	2 AH1512	hypothetical prote
22	47	34.1	227	2 E75066	hypothetical prote
23	47	34.1	445	2 B75558	probable translati
24	47	34.1	465	2 H87636	acetyl-CoA carboxy
25	47	34.1	697	2 T03834	glutamine syntheta
26	47	34.1	761	2 S61642	nucleic distributi
27	46.5	33.7	453	2 S38966	translation elonga
28	46.5	33.7	543	2 T34481	hydroxymethylgluta
29	46.5	33.7	1964	2 T09059	hypothetical prote
					notch4 - mouse

30	46	33.3	124	2 AF0088	hypothetical prote
31	46	33.3	190	2 A88961	protein F59A7.4 li
32	46	33.3	205	2 I46876	phosphoprotein pho
33	46	33.3	482	2 S75847	signal recognition
34	46	33.3	554	2 F66244	hypothetical prote
35	46	33.3	560	2 S53382	protein YKR029c ho
36	46	33.3	574	2 T51799	CtA1-like protein
37	46	33.3	710	2 F66778	DNA topoisomerase
38	46	33.3	727	2 AD2168	hypothetical prote
39	46	33.3	757	1 S48841	secretory componen
40	46	33.3	757	2 I45956	polymeric immunogl
41	46	33.3	1103	2 JC4114	Ca2+-transporting
42	46	33.3	1612	2 AB1347	probable peptidogl
43	46	33.3	2254	2 DB6215	protein T6D22.14 l
44	45.5	33.0	253	2 T37247	histone H1.4 - Cae
45	45.5	33.0	253	2 F69030	protein C18G1.5 l

ALIGNMENTS

RESULT 1

T34061

hypothetical protein F28B3.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T34061

R:Geisels, C.; Kramer, J.; Smith, A.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid F28B3.

A:Reference number: Z21469

A:Accession: T34061

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1394 <GB>

A:Cross-references: UNIPROT:O01787; EMBL:AF003136; PIDD:AA093633.1; GSPDB:GN00019; CESP:

A:Experimental source: strain Bristol N2; clone F28B3

C:Genetics:

A:Gene: CESP:F28B3.1

A:Map position: 1

A:Introns: 46/3; 105/2; 280/3; 337/1; 358/1; 530/3; 685/3; 789/3; 1311/2

Query Match 38.4%; Score 53; DB 2; Length 1394;

Best Local Similarity 40.9%; Pred. No. 67;

Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

3 EKIKTTVKESATEBKLTPLVLA 24

Db 1370 EKIKTTVKESATEBKLTPLVLA 1391

RESULT 2

B71931

DNA gyrase chain B - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Title: strain J99

A:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: B71931

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-773 <ARN>

A:Cross-references: UNIPROT:Q9ZLX3; GB:AE001479; GB:AE001439; NID:g4154979; PIDD:AA0603

A:Experimental source: strain J99

C:Genetics:

A:Gene: gyrB

C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match	37.0%	Score 51	DB 2	Length 773
Best Local Similarity	43.5%	Pred. No. 65		
Matches	10	Conservative	6	Mismatches 7
				Indels 0
				Gaps 0
QY	5	IKTYKESATBEKLTPLVLAQOL	27	
	:	:: :: ::	:	
Db	222	LKQFVDSAKKELLPTLIAFSM	244	

RESULT 3

penicillin-binding protein (pbp-3) homolog - Lyme disease spirochaete
C:Species: *Borrelia burgdorferi* (Lyme disease spirochaete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: C70191
R:Risser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whitte-
son, D.; Peterson, J.; Kurlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugr-
; Bowman, C.; Garland, J.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nucleus 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: C70191
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-932 <KLE>
A:Cross-references: UNIPROT:O51674; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AC6708
A:Experimental source: strain B31

Query Match	Score 51;	DB 2;	Length 932;
Best Local Similarity	37.0%	37.0%	91.

Best local similarity 37.38; Freq. NO. 81;
Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

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Qy      2 VEKIKTVKESATEEKLTPVLLAKQAL 30
      ::||| :||| |:| :|
Db      397 IDKIDKATKEYIINKNLTPLKIAQPEGAM 425
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RESULT 4

I:lipote-protein:lipase B (lipote biosynthesis protein B) [imported] - Salmonella enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: This species has also been called Salmonella typh
 C:Date: 09-Nov-2002 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AF0580
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0580
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-191 <PAR>
 A:Cross-references: GB:ALU513382; PIDN:CAD05112.1; PID:G16501886; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY0686
 C:Superfamily: Escherichia coli lipote-protein lipase 11pb

Query Match	36.6%	Score 50.5;	DB 2;	Length 191;
Best Local Similarity	50.0%;			
Matches 15; Conservative	3;	Pred. No. 17;		
		Mismatches 11;		Indels 1;
				Gaps 1;

```

QY      1 EVEKIKTTVESATEEKTLPVLLAKQLAAL 30
      | : | | | | | : | | | | |
Db    153 EMAKI-TQWKEDATTTDNIAPRLANILALI 18

```

RESULT 5

hypothetical protein At2g11890 [imported] - Arabidopsis thaliana

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004

Accession: E84499
Rilim, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Unayam, L.; Tallon, L.; Euse, D.; Nieman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

Article: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
Reference number: A84420; NCBI:20083487; PMID:10617197

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-210 <ST

A;Cross-references: U
C;Genetics:

A;Gene: At2g11890
A;Map position: 2

C;Supertamily: unchar

Query Match
Best Local Similarity

Matches 9; CONE

QY I EWEKIKI
| | :: ||
| | :: ||

ДБ 174 ЕРЕРВК1

RESULT 6

DNA gyrase, sub B - Helicobacter pylori (strain 26695)
C|Species: Helicobacter pylori
C|Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C|Accession: E64582
R|Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 368, 539-547, 1997
A|Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Frazer, C.
A|Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A|Reference number: A64520; MUID:97394467; PMID:9252185
A|Accession: E64582
A|Status: preliminary; nucleic acid sequence not shown; translation not shown
A|Molecule type: DNA
A|Residues: 1-773 <TOMB>
A|Cross-References: UNIPROT:P55992; GB:AE000564; GB:AE000511; NID:g2313602; PIDD:AA0756
C|Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match 36.2%; Score 50; DB 2; Length 773;

Best Local Similarity 43.5%; Pred. No. 90;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 5 IKTIVKESATEEKLTPVLLAKÖL 27
:|:|:|:|:|:|:|:
Db 222 LKÖFVKDSAKKELTPITISFKSM 244

RESULT 7

hypothetical protein DKFZ5860917.1 - human (fragment)
 C|Species: Homo sapiens (man)
 C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C|Accession: T17245
 R|Kocher, K.; Beyer, A.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A|Reference number: Z18722
 A|Accession: T17245
 A|Status: preliminary
 A|Molecule type: mRNA
 A|Residues: 1-878 <KOE>
 A|Cross-references: EMBL:AL117455
 A|Experimental source: adult uterus; clone DKFZ5860917
 C|Genetics:

A>Note: DKFZp586J0917.1

Query Match 36.2%; Score 50; DB 2; Length 878;
Best Local Similarity 44.0%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 KTTVESATTEKLTPTVLAKQAL 30
DB 3 RSAVSSVVKQLAELVILKQQAAL 27

RESULT 8

AG1717

probable peptidoglycan bound protein (LPXG motif) lin2283 [imported] - *Listeria innocua*
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG1717

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguer, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karsc, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, O.K.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1717

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1151 <GAA>

A:Cross-references: UNIPROT:Q929J2; GB:AL592022; PIDN:CA697511.1; PID:gl6414795; GSPDB:C

A:Experimental source: strain C11p1262

C:Genetics:

A:Gene: lin2283

Query Match 36.2%; Score 50; DB 2; Length 1151;
Best Local Similarity 58.8%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EKIKTVESATTEKLT 19
DB 31 EGVETNVEATTEKVT 47

RESULT 9
B82707
carboxyphosphoenolpyruvate phosphonmutase XF1234 [imported] - *Xylella fastidiosa* (str

C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: B82707

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: AB2515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number AS9328 below

A:Accession: B82707

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <SIM>

A:Cross-references: UNIPROT:Q9P24; GB:AE003957; GB:AE003849; NID:g9106207; PIDN:AAF8404

A:Experimental source: strain 945C

R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

A:Contents: annotation

C:Genetics:

C:Species: XF1234

C:Superfamily: carboxyphosphoenolpyruvate phosphonmutase

Query Match 35.5%; Score 49; DB 2; Length 298;
Best Local Similarity 41.4%; Pred. No. 44;
Matches 12; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 VEKIKTVESATTEKLTPTVLAKQAL 30
DB 204 VERTRPVPLAMTEFGKTPILTRQLEAV 232

RESULT 10
T42684
hypothetical protein DKFZp434F232.1 - human (fragment)

C:Species: *Homo sapiens* (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42684

R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22233

A:Accession: T42684

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-340 <AAA>

A:Cross-references: UNIPROT:Q96MK3; EMBL:AL133105

A:Experimental source: adult testis; clone DKFZp434F2322

C:Genetics:

A>Note: DKFZp434F2322.1

Query Match 35.5%; Score 49; DB 2; Length 340;
Best Local Similarity 37.0%; Pred. No. 51;
Matches 10; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 KIKTVESATTEKLTPTVLAKQAL 30
DB 271 RLSDVMRESLLELDQSLPVLTEPHLAL 297

RESULT 11
B71480
probable agx-1 homolog-udp-glucose pyrophosphorylase - *Chlamydia trachomatis* (serotype T

C:Species: *Chlamydia trachomatis*
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: B71480

R:Stephens, R.S.; Kalman, S.; Lammel, C.D.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trac*

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: B71480

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <ARN>

A:Cross-references: UNIPROT:O84720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT715

Query Match 35.5%; Score 49; DB 2; Length 455;
Best Local Similarity 46.2%; Pred. No. 70;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 IKTTVESATTEKLTPTVLAKQAL 30
DB 264 IKTTROSAQEDVGLILAKQITAV 289

RESULT 12

IO8544

primosome component (helicase loader) dnaI - *Bacillus subtilis*

A:Title: The

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: B71480

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <ARN>

A:Cross-references: UNIPROT:O84720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT715

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <ARN>

A:Cross-references: UNIPROT:O84720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT715

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <ARN>

A:Cross-references: UNIPROT:O84720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT715

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <ARN>

A:Cross-references: UNIPROT:O84720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT715

C/Species: Bacillus subtilis
C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: B24720; C26580; F69617
R/Ogasawara, N.; Moriya, S.; Maza, P.G.; Yoshikawa, H.
Nucleic Acids Res. 14, 9989-9999, 1986
A/Title: Nucleotide sequence and organization of dnaB gene and neighbouring genes on the
A/Reference number: A93650; MUID:87117549; PMID:3027671
A/Accession: B24720
A/Molecule type: DNA
A/Residues: 1-311 <OGA>
A/Cross-references: UNIPROT:P06567; GB:X04963; NID:939880; PIDN:CAA28633.1; PID:939881
R/Hoshino, T.; McKeen, T.; Schmitz, S.; Tanaka, T.; Sueoka, N.
Proc. Natl. Acad. Sci. U.S.A. 84, 653-657, 1987
A/Title: Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for DNA replica
A/Reference number: A94709; MUID:87118226; PMID:3027697
A/Accession: C26580
A/Molecule type: DNA
A/Residues: 1-18, 'N', 20-23, 'T', 25-206 <HOS>
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Busch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
leech, J.; Harwood, C.R.; Henaui, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Autors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, V.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetall
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanlon,
A.; Autors: Schleich, S.; Schroefer, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: F69617
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-311 <KUN>
A/Cross-references: GB:Z99118; GB:AL009126; NID:92635200; PIDN:CAB14858.1; PID:92635363
A/Experimental source: strain 168
C/Genetics:
A/Gene: dnaI
C/Superfamily: 44K dnaA protein homolog
C/Keywords: ATP; nucleotide binding; P-loop
F:168-175/Region: nucleotide-binding motif A (P-loop)
Query Match 35.1%; Score 48.5; DB 1; Length 311;
Best Local Similarity 33.3%; Pred. No. 54;
Matches 11; Conservative 8; Mismatches 9; Indels 5; Gaps 1;
Oy 2 VEKIKTVKESATEKLT-----TPVLAKQLAA 29
Db 201 VRELKNSLDQDTLEKLMNMTTPVLMDDIGA 233
RESULT 13
T52431
hypothetical protein ZCF37 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52431
R/Kato, A.; Suiki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.
Gene 239, 309-316, 1999
A/Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg
A/Reference number: Z25171
A/Accession: T52431
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-211 <KAT>
A/Cross-references: UNIPROT:Q9SLT9; EMBL:AB028223; PIDN:BA87954.1
A/Experimental source: cultivar Columbia
C/Genetics:
A/Map position: 1

A/Note: ZCF37
Query Match 34.8%; Score 48; DB 2; Length 211;
Best Local Similarity 64.3%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 3 EKIITVKSATEE 16
Db 91 DKVTEVKEATEE 104
RESULT 14
T34100
hypothetical protein C17G10.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34100
R/Johnson, D.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid C17G10.
A/Reference number: Z21476
A/Accession: T34100
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-379 <JOH>
A/Cross-references: UNIPROT:Q09974; EMBL:U28739; PIDN:AA93452.1; GSPDB:GN00020; CESP:CI
A/Experimental source: strain Bristol N2; clone C17G10
C/Genetics:
A/Gene: CESP:C17G10.2
A/Map position: 2
A/Introns: 36/3; 81/1; 167/1; 252/3; 355/3
Query Match 34.8%; Score 48; DB 2; Length 379;
Best Local Similarity 32.1%; Pred. No. 79;
Matches 9; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
Oy 2 VEKIKTVKESATEKLTTPVLAKQLAA 29
Db 75 IEALQASIKENSPRKLMNAVLYFRANA 102
RESULT 15
D75056
cell division control protein. PAB2373 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: D75056
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A/Reference number: A75001
A/Accession: D75056
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1112 <RAW>
A/Cross-references: UNIPROT:Q09YR7; GB:A248287; GB:AL096836; NID:95458657; PIDN:CAB5034
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: cdc21; PAB2373
Query Match 34.8%; Score 48; DB 2; Length 1112;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 11; Mismatches 4; Indels 6; Gaps 3;
Oy 1 EVE---KIKTVKESATEKLTTPVLAKQLAA 30
Db 958 EIEKYVMKRSVKKS-SEERIKPIPTARQLEAL 991
Search completed: November 3, 2005, 22:04:14
Job time : 11.9091 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 ; Search time 91.4866 Seconds
(without alignments)
291.060 Million cell updates/sec

Title: 09782816-51

Sequence: 1 GVKETPOOKYORLHEVQEL.....ESATBEKLPVILAKQIALAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	100.0	400	1 DCT2_HUMAN	Q13561 homo sapien
2	248	98.8	401	1 DCT2_MOUSE	Q99KJ8 mus musculu
3	248	98.8	402	1 O6AYH5	Q6ayh5 rattus norv
4	220	87.6	403	2 O6IRB3	Q6irb3 xenopus lae
5	213	84.9	403	2 O66J30	Q66j30 xenopus lae
6	211	84.1	338	2 O7ZXY2	Q7zxy2 xenopus lae
7	177	70.5	402	2 O9PTG6	Q9ptg6 gallus gall
8	177	70.5	405	2 O7T3H1	Q7t3h1 brachydanio
9	76	30.3	402	2 O6IP53	Q6ip53 xenopus lae
10	72.5	28.9	380	2 O9V4Y9	Q9v4y9 drosophila
11	71	28.3	800	2 O6MVP7	Q6mvp7 neurospora
12	71	28.3	813	2 O7SH14	Q7sh14 neurospora
13	70	27.9	311	2 O97IY5	Q97iy5 sulfolobus
14	70	27.9	751	2 O8MQK1	Q8mqk1 drosophila
15	70	27.9	1087	2 O8BBS5	Q8bbs5 drosophila
16	70	27.9	1124	2 O8MQJ8	Q8mqj8 drosophila
17	70	27.9	2199	2 O7PUP2	Q7pup2 anopheles g
18	69.5	27.7	873	2 O9SXS5	Q9sxs5 caenorhabdi
19	69.5	27.7	919	2 O9SXS5	Q9sxs5 caenorhabdi
20	68	27.1	1755	2 O7RV31	Q7rv31 neurospora
21	68	27.1	1968	2 O8XOC5	Q8xoc5 neurospora
22	67.5	26.9	1868	2 O6BNV2	Q6bnv2 debrayomyce
23	67	26.7	455	2 O7ZVFL	Q7zvf1 brachydanio
24	67	26.7	639	2 O6Z245	Q6z245 caenorhabdi
25	67	26.7	1795	2 O9LCI9	Q9lcj9 staphylococ
26	67	26.7	2478	2 O9LCH2	Q9lch2 staphylococ
27	67	26.7	2478	2 O9RL69	Q9rl69 staphylococ
28	67	26.7	2481	2 O99QR6	Q99qr6 staphylococ
29	67	26.7	2481	2 O7A4B1	Q7a4b1 staphylococ
30	66	26.3	393	2 O49567	Q49567 arabidopsis
31	66	26.3	860	2 O7Q0Q9	Q7q0q9 anopheles g

32	66	26.3	866	2 O84500	O84500 chlamydia t
33	66	26.3	1022	2 O8TBV8	O8tbv8 homo sapien
34	65.5	26.1	1837	2 O74424	O74424 schizosach
35	65	25.9	388	2 Q7PZ25	Q7pz25 anopheles g
36	64.5	25.7	348	2 O8LIJ9	O8lij9 oryza sativ
37	64	25.5	149	2 O9BZS3	O9bz33 homo sapien
38	64	25.5	188	2 O9UM00	O9um00 homo sapien
39	64	25.5	188	2 O921L3	O921l3 mus musculu
40	64	25.5	188	2 O6DGM9	O6dgm9 brachydanio
41	64	25.5	210	2 O98IY3	O98iy3 arabidopsis
42	64	25.5	230	2 O75545	O75545 homo sapien
43	64	25.5	1227	1 JIP3_DROME	JIP3_drome
44	64	25.5	1956	2 O9Y2K3	O9y2k3 homo sapien
45	63.5	25.3	163	1 Y012_BPBP1	Y012_bpbp1 bacterioph

ALIGNMENTS

RESULT 1

DCT2_HUMAN

AC Q13561; O86YN2; Q9BW17; ID 01-NOV-1997 (Rel. 35, Created) PRT; 400 AA.

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide) (p50 dynactin) (DCTN-50) (Dynactin 2).

OS Homo sapiens (Human);

GN Name=DCTN2; Synonyms=DCTN50;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

11

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=96178072; PubMed=8647893; DOI=10.1083/jcb.132.4.617;

RA Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;

RT "Molecular characterization of the 50-kD subunit of dynactin reveals function for the complex in chromosome alignment and spindle organization during mitosis.";

RT J. Cell Biol. 132:617-633(1996).

12

RN SEQUENCE FROM N.A.

RP TISSUE=Placenta, Skin, and Uterus;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Stromberg R.L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,

RA Ditchenko L., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stromstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,

RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Roach S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,

RA Vallay D.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,

RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

13

RN SEQUENCE OF 1-384 FROM N.A.

RP Aumais J.P., Yu-lee L.-Y.;

RT "Human 50 kD dynactin subunit, p50 dynactin, isolated from HeLa cells.";

RT Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.

14

SEQUENCE OF 1-13.

CC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/rbce810;
 RA Gervart K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.,
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides";
 RL Nat. Biotechnol. 21:566-569(2003).
 CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
 CC and plays a role in prometaphase chromosome alignment and spindle
 CC organization during mitosis. May play a role in synapse formation
 CC during brain development.
 CC -1- SUBUNIT: Subunit of dyneactin, a multiprotein complex associated
 CC with dynein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
 CC
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC EMBL; U50733; AAC0423.1; -;
 DR EMBL; BC000718; AAH00718.1; -;
 DR EMBL; BC0009468; AAH09468.1; -;
 DR EMBL; BC014083; AAH14083.1; -;
 DR EMBL; AY189155; AAC034395.1; -;
 DR Genew; H8NC:2712; DCTN2.
 DR MIM; 607376; -;
 DR GO; GO:0005813; C:centrosome; TAS.
 DR GO; GO:0005869; C:dyneactin complex; TAS.
 DR GO; GO:0000776; C:kinetochore; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007067; P:mitosis; TAS.
 DR InterPro; IPR006996; Dyneactin.
 DR Pfam; PF04912; Dyneactin; 1.
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
 KW Membrane; Microtubule; Motor protein.
 FT INIT MET 0
 FT DOMAIN 98 131 Coiled coil (Potential).
 FT DOMAIN 213 243 Coiled coil (Potential).
 FT DOMAIN 378 398 Coiled coil (Potential).
 FT CONFLICT 34 34 A -> APAQL (in Ref. 1).
 FT CONFLICT 35 35 E -> ELE (in Ref. 3).
 FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).
 SQ SEQUENCE 400 AA; 44099 MW; 0A95A895C0B8270F CRC64;

Query Match 100.0%; Score 251; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 4.7e-17;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKTPQOKYQRLHVEVQLTTEVEKITTKTKESITTEKLTPLVLAQOLAL 52
 DB 93 GYKTPQOKYQRLHVEVQLTTEVEKITTKTKESITTEKLTPLVLAQOLAL 144

RESULT 2

DCT2_MOUSE STANDARD; PRT; 401 AA.
 AC Q99KJ8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Dyneactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
 DE (p50 dyneactin) (DCTN-50) (Dyactin 2) (Growth cone membrane protein
 DE 23-48K) (GMP23-48K).
 GN Name=Dctn2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
 RA Klusner R.D., Collins F.S., Wagner L., Sherman C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA DiCicco L., Maris N.K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stetson M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toehlyuk S., Carninci P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Bikerley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,
 RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC TISSUE=Brain;
 RX MEDLINE=97289622; PubMed=9144527; DOI=10.1006/dbnc.1997.6447;
 RA Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.;
 RT "The presence of the 50-kDa subunit of dyneactin complex in the nerve
 RT growth cone";
 RL Biochem. Biophys. Res. Commun. 233:295-299(1997).
 RN [3]
 RP INTERACTION WITH BICD2.
 RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
 RA Hoogenraad C.C., Akhmanova A., Howell S.A., Portland B.R.,
 RA de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.;
 RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-
 RT dyneactin pathway by interacting with these complexes";
 RL EMBO J. 20:4041-4054(2001).
 CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
 CC and plays a role in prometaphase chromosome alignment and spindle
 CC organization during mitosis. May play a role in synapse formation
 CC during brain development.
 CC -1- SUBUNIT: Subunit of dyneactin, a multiprotein complex associated
 CC with dynein (By similarity). Interacts with BICD2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
 CC -1- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic
 CC and membrane-associated forms in neonates. Levels of membrane-
 CC associated form are greatly reduced in the adult.
 CC
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 CC or send an email to license@sib-sib.ch).

CC EMBL; BC004613; AAH04613.1; -;
 DR MGD; MGI:107733; Dctn2.
 DR InterPro; IPR006996; Dyneactin.
 DR Pfam; PF04912; Dyneactin; 1.
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
 KW Membrane; Microtubule; Motor protein.
 FT INIT MET 0
 FT DOMAIN 98 131 Coiled coil (Potential).
 FT DOMAIN 214 244 Coiled coil (Potential).
 SQ SEQUENCE 401 AA; 43985 MW; 153584ABD5940EBC CRC64;

Query Match 98.8%; Score 248; DB 1; Length 401;
 Best Local Similarity 98.1%; Pred. No. 9.4e-17;
 Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 52
 DB 93 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 144

RESULT 3
 ID 06AVH5 PRELIMINARY; PRT; 402 AA.
 AC 06AVH5.
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Dynactin 2.
 GN Name=Dctn2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL: BC079042; AAH79042.1; -
 DR GO: GO:0005869; C:dynactin complex; IEA.
 DR GO: GO:0007017; P:microtubule-based process; IEA.
 DR InterPro: IPR006996; Dynamitin.
 DR Pfam: PF04912; Dynamitin; 1.
 SQ SEQUENCE 402 AA; 44148 MW; 55033555A4FB052 CRC64;

Query Match 98.8%; Score 248; DB 2; Length 402;
 Best Local Similarity 98.1%; Pred. No. 9.4e-17;
 Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 52
 DB 94 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 145

RESULT 4
 ID 06IRB3 PRELIMINARY; PRT; 403 AA.
 AC 06IRB3.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Dctn2-prov protein.
 GN Name=dctn2-prov;
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX Klein S., Strausberg R.;
 RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL: BC070987; AAH70987.1; -
 DR GO: GO:0005869; C:dynactin complex; IEA.
 DR GO: GO:0007017; P:microtubule-based process; IEA.
 DR InterPro: IPR006996; Dynamitin.
 DR Pfam: PF04912; Dynamitin; 1.
 SQ SEQUENCE 403 AA; 44828 MW; 9FD158C7C7983062 CRC64;

Query Match 87.6%; Score 220; DB 2; Length 403;
 Best Local Similarity 84.6%; Pred. No. 6e-14;
 Matches 44; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 52
 DB 94 GVKETPOOKYORLHEVOELTTEVEKITTVEKESATEKRLPVLLAKOLAL 145

RESULT 5
 ID 06CJ30 PRELIMINARY; PRT; 403 AA.
 AC 06CJ30.
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE MGC82128 protein.
 GN Name=MGC82128;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8335;
 RN [1]

RA SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12479932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinchi P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerthard D.S.,
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081081; AAH81081.1;
DR InterPro; IPR006996; Dynamitin.
DR Pfam; PF04912; Dynamitin; 1.
SQ SEQUENCE 403 AA; 44737 MW; 86B8CBE54325EF3 CRC64;

Query Match 84.9%; Score 213; DB 2; Length 403;
Best Local Similarity 82.7%; Pred. No. 3e-13;
Matches 43; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 GVKTPOQKRYRLHVEOELTTEVEKIKTTVKESATREKLTPLVALAKQALAL 52
DB 94 GKMETPOQKRYRLHVEOELTTEVEKIKTTVKESATREKLTPLVALAKQVAST 145

RESULT 6
O7ZXV2 PRELIMINARY; PRT; 338 AA.
AC O7ZXV2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Dcun2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinchi P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044069; AAH44069.1;
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynamitin.
DR Pfam; PF04912; Dynamitin; 1.
SQ SEQUENCE 338 AA; 38257 MW; 3346E0F0F644B186 CRC64;

Query Match 84.1%; Score 211; DB 2; Length 338;
Best Local Similarity 86.0%; Pred. No. 4e-13;
Matches 43; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 KETPOQKRYRLHVEOELTTEVEKIKTTVKESATREKLTPLVALAKQALAL 52
DB 31 KETPOQKRYRLHVEOELTTEVEKIKTTVKESATREKLTPLVALAKQVAST 80

RESULT 7
O9PTG6 PRELIMINARY; PRT; 402 AA.
AC O9PTG6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Dynamitin.
GN Name=p50;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20056093; PubMed=10588646;
RX Valetti C., Metzel D.M., Schrader M., Hasbani M.J., Gill S.R.,
RA Kreis T.E., Schroer T.A.,
RT "Role of dynactin in endocytic traffic: effects of dynamitin
RT overexpression and colocalization with CLIP-170.";
RL Mol. Biol. Cell 10:4107-4120(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC Schroer T.A., Gill S.R., Hasbani J., Grego C.,
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200744; AAF13996.1;
DR GO; GO:0005869; C:dynactin complex; IEA.

DR	GO; GO:0007017; P:microtubule-based process; IEA.
DR	InterPro; IPR006996; Dynamitin.
DR	Pfam; PF04912; Dynamitin; 1.
SO	SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;
Qy	Query Match 70.5%; Score 177; DB 2; Length 402; Best Local Similarity 67.3%; Pred. No. 1.2e-09; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0
Db	1 GVSETPPOKYRORLHEVOELITTEVEKIKTTYSATEEKLTPVLAKOLAL 52 96 GAKETPPOKYRORLHEVOELIRVDIOISAVKESAABEBETPMALAROLEGL 147
RESULT 8	
ID Q7T3H1	PRELIMINARY; PRT; 405 AA.
AC Q7T3H1	
DT 01-OCT-2003 (TREMBLrel. 25, Created)	
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)	
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DE Similar to dynactin 2 (P50).	
GN ORFNames=zgc:63867;	
OS Brachydanio rerio (zebrafish) (Danio rerio).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC Cyprinidae; Danio.	
OX NCBI_TaxId=7955;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Embryo;	
RX MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Butler K.H., Schaefer C.J.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Mak S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., Stadleren M., Soares M.B., Bonaldo M.F., Cavavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J., Maiz M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."	
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RL [2]	
RN SEQUENCE FROM N.A.	
RP TISSUE=Embryo;	
RC Strausberg R.;	
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.	
DR EMBL; BC053120; AAHS3120.1; -.	
DR ZFIN; ZDB-GENE-040426-1279; zgc:63867.	
DR GO; GO:0005869; C:dynactin complex; IEA.	
DR GO; GO:0007017; P:microtubule-based process; IEA.	
DR InterPro; IPR006996; Dynamitin.	
DR Pfam; PF04912; Dynamitin; 1.	
SO SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;	
Qy	Query Match 70.5%; Score 177; DB 2; Length 405; Best Local Similarity 67.3%; Pred. No. 1.2e-09; Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0
Db	1 GVSETPPOKYRORLHEVOELITTEVEKIKTTYSATEEKLTPVLAKOLAL 52 96 GVSETPPOKYRORLHEVOELITTEVEKIKTTYSATEEKLTPVLAKOLAL 147

	RESULT	9
ID	Q61P53	PRELIMINARY; PRT; 402 AA.
AC	Q61P53;	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE	MGC78949 protein.	
CN	Name=MGC78949;	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	
OX	NCBI_TaxID=8355;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RX	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Aleschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,	
RA	Datchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulik S.W.,	
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Nelson E., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodríguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywnicki M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Maiz M.A.?	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).	
RN	[2]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=Embryo;	
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;	
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,	
RA	Richardson P.;	
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus	
RT	initiative."	
RL	Dev. Dyn. 225:384-391(2002).	
RN	[3]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=Embryo;	
RC	Klein S., Strausberg R.;	
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; BC072065; AAAH2065.1;	
DR	GO; GO:0005874; C:microtubule; IEA.	
DR	GO; GO:0002262; P:microtubule cytoskeleton organization and b. . . ; IEA.	
DR	InterPro; IPR000435; Teklin.	
DR	Pfam; PF03148; Teklin; 1.	
DR	PRINTS; PR00511; TEKTLIN.	
SO	SEQUENCE 402 AA; 46535 MW; FI73BC4BFC0E798A CRC64;	
Query March	30.3%; Score 76; DB 2; Length 402;	
Best Local Similarity	46.4%; Pred. No. 16;	
Matches 13; Conservative	10; Mismatches 5; Indels 0; Gaps 0;	
QY	12 RLHEVQLTEVEKIKTYVESATEEK 39	
DB	336 RLINVEOITTNIRLETLGQARTLK 363	
RESULT 10		
ID Q9V4Y9	PRELIMINARY; PRT; 380 AA.	

AC O9V4Y9 : 01-MAY-2000 (Tremblurel_13, Created)

DT 01-MAY-2000 (Tremblurel_13, Last sequence update)

DT 25-Oct-2004 (Tremblurel_28, Last annotation update)

DE CG8269-PA (LD07994P).

GN Name=Dmn; ORFNames=CG8269;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

OC Ephydroidea, Drosophilidae, Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=19196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goeys J.D.,

RA Aamstad P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Branton R.C., Rogers Y.H., Blazynski R.G., Chang M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,

RA Abail J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

RA Ballew R.M., Baau A., Bakendell J., Bayreuth-Pfannkuch C., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bernan B.P., Bhattacharya D., Bolshakov S.,

RA Borkova D., Borchen M.R., Bouck J., Brodeur P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cateley S., Dahlke C., Davenport L.B., Davies P.,

RA de Palos B., Deitcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,

RA Jostai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.M., Nelson K.A., Nixon K.A., Nusser D.R., Pacle J.M.,

RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puti V., Reese M.G.,

RA Reinhart K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.F., Smith T.,

RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodagel, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu K., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S.J., Adams M., Champ M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stepleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kronmiller B., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin

RT a genome perspective.";

RL Genome Biol 3:RESEARCH0084-RESEARCH0084(2002).

[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Miranda S., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupry J.L., Whittied S.E., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Gelinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Ruso S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rudin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RN SEQUENCE FROM N.A.
RG Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RG Flybase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuccio J., Paolel J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Gelinker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003835; AA059034.1; -
DR EMBL; AY061092; AAL28640.1; -
DR InFact; Q9V4Y9; -
DR Flybase; FBgn0021825; Dmn.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006966; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
SQ SEQUENCE 380 AA; 41998 MW; CF7E1D3BFF5989C5 CRC64;

Query Match 28.9%; Score 72.5; DB 2; Length 380;
Best Local Similarity 48.7%; Pred. No. 34;
Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 GVKETPOQKQYRLAHEVOELTTEVEKIKTKVKSATEEK 39
DB 94 GKETPVQKQRLQIEMNELNEVALQVD-RKVADDEK 131

RESULT 11
GEMVP7
ID 06MVP7. PRELIMINARY; PRT; 800 AA.
AC 06MVP7.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Probable translation elongation factor EF-G, mitochondrial.
GN Name=B16D18.090;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
OX RN [1]
RN SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX842625; CAF76249.1; -
DR GO; GO:0005525; F:GTP binding; IEA

```
DR GO: GO:0003746; P:translation elongation factor activity; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0006414; P:translational elongation; IEA.
DR InterPro: IPR004540; EF-G.
DR InterPro: IPR000640; ERG_C.
DR InterPro: IPR003022; ERG_III_V.
DR InterPro: IPR005517; ERG_IV_.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR000795; ProTSyn_GTPbind.
DR InterPro: IPR005225; Small_GTP.
DR InterPro: IPR003000; Translat_factor.
DR Pfam: PF00679; ERG_C; 1.
DR Pfam: PF03764; ERG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATINCT.
DR TIGRFAMs: TIGR00484; EF-G; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
DR PROSITE: PS00301; EFACROR_GTP; 1.
KW Elongation factor; GTP-binding; Protein biosynthesis.
SQ SEQUENCE 800 AA; 88373 MW; F2A7C425F6D4974A CRC64;

Query Match 28.3%; Score 71; DB 2; Length 800;
Best Local Similarity 26.2%; Pred. No. 1e+02;
Matches 16; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 2 VKETPQOKYORLLHEVOELTTEV-----EKIKTTVKESATEEKLTPVYLAKQL 49
DB 306 IKELCEQKQRELIKLVADVDDEIEMFLEBQTPPEQIKAIRATYACKTKTPVLMGSAI 365

QY 50 A 50
DB 366 A 366

RESULT 12
Q7SH14 PRELIMINARY; PRT; 813 AA.
ID Q7SH14
AC Q7SH14;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02955.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0874A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iannelli P., Pedersen D., Nelson M., Washburne M.,
RA Selfetrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyssejls M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krysiofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
RL Nature 0-0(12003).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX0100006; EAA36106.1; -.
DR HSSP: P13551; 1FNM.
DR GO: GO:0005525; P:GTP binding; IEA.
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DR GO: GO:0003746; P:translation elongation factor activity; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0006414; P:translational elongation; IEA.
DR InterPro: IPR004540; EF-G.
DR InterPro: IPR000640; ERG_C.
DR InterPro: IPR003022; ERG_III_V.
DR InterPro: IPR005517; ERG_IV_.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR000795; ProTSyn_GTPbind.
DR InterPro: IPR005225; Small_GTP.
DR InterPro: IPR003000; Translat_factor.
DR Pfam: PF00679; ERG_C; 1.
DR Pfam: PF03764; ERG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATINCT.
DR TIGRFAMs: TIGR00484; EF-G; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
DR PROSITE: PS00301; EFACROR_GTP; 1.
KW GTP-binding; Hypothetical protein; Protein biosynthesis.
SQ SEQUENCE 813 AA; 89810 MW; C9A5093F35B29B05 CRC64;

Query Match 28.3%; Score 71; DB 2; Length 813;
Best Local Similarity 26.2%; Pred. No. 1e+02;
Matches 16; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 2 VKETPQOKYORLLHEVOELTTEV-----EKIKTTVKESATEEKLTPVYLAKQL 49
DB 306 IKELCEQKQRELIKLVADVDDEIEMFLEBQTPPEQIKAIRATYACKTKTPVLMGSAI 365

QY 50 A 50
DB 366 A 366

RESULT 13
Q971V5 PRELIMINARY; PRT; 311 AA.
ID Q971V5
AC Q971V5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein S71273.
GN OrderedLocustNames=S71273;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anrai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.",
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000985; BAB6315.1; -.
DR HSSP: P01100; 1FOS.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 311 AA; 37536 MW; 674338A5E031B429 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 311;
Best Local Similarity 35.3%; Pred. No. 50;
Matches 18; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

QY 2 VKETPQOKYORLLHEVOELTTEVEKIKTTVKESATEEKLTPVYLAKQLAAL 52
DB 71 IKOLSQOK-OSLIQVISEIKKEFEQIKNVEK---VKKELDPLQILTKIEQL 117
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RESULT 14
ID Q8MOK1 PRELIMINARY; PRT; 751 AA.
AC Q8MOK1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
GN l008185p
ORFNames=CG10971;
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Abghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY129439; AAM76181.1; -.
DR FlyBase: FBgn0036309; CG10971.
DR GO: GO:0003779; F:actin binding; IEA.
DR InterPro: IPR002558; ILMQ.
DR Pfam: PF01608; I_LMQ; 1.
DR PROSITE: PS50945; I_LMQ; 1.
SQ SEQUENCE 751 AA; 85362 MW; 7E9BC7661ECB8A0 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 751;
Best Local Similarity 44.2%; Pred. No. 1.2e+02;
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

OY 7 QOKYORLHEVOELTTEVEKIKTKYKESATSEKLTPLVLAQQL 49
Db 72 KQVNSQLLTKETLTKETLTKIKVNE--KPK-TNLTLOKQI 110

RESULT 15
ID Q8GBS5 PRELIMINARY; PRT; 1087 AA.
AC Q8GBS5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
GN CG10971-PB.
ORFNames=CG10971;
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RL MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Abghayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Bendable J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaisl M., Kallush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537558;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
[5]
RN
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
[6]
RN
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB003540; AAF49884.1; -.
DR FlyBase: FBgn0036309; CG10971.
DR GO: GO:0003779; F:actin binding; IEA.
DR GO: GO:0005543; F:phospholipid binding; IEA.
DR InterPro: IPR01417; ANTH.
DR InterPro: IPR001026; Epsin_N.

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DR InterPro; IPR002558; ILMEQ.
 DR InterPro; IPR008943; PI_bind_N.
 DR Pfam; PF07651; ANTH; 1.
 DR Pfam; PF01608; I_LMEQ; 1.
 DR ProDom; PD01820; ILMEQ; 1.
 DR ProSite; PS50942; ENTH; 1.
 DR ProSite; PS50945; I_LMEQ; 1.
 SQ SEQUENCE 1087 AA; 124298 MW; C83E709907DFE8E8 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 1087;
 Best Local Similarity 44.2%; Pred. No. 1.8e+02;
 Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

QY 7 QQKTRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:51:39 ; Search time 26.6952 Seconds
(without alignments)
145,410 Million cell updates/sec

Title: 09782816-51
Perfect score: 251
Sequence: 1 GVKETPOOKYQRLHEVQEL.....ESATEEKLTPLAKQIALAL 52

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	26.3	142	4	US-09-270-767-43370 Sequence 43370, A
2	64.5	25.7	639	4	US-09-902-540-14908 Sequence 14908, A
3	64	25.5	151	4	US-09-513-999C-7806 Sequence 7806, Ap
4	64	25.5	193	4	US-09-107-532A-5587 Sequence 5587, Ap
5	63	25.1	850	4	US-09-269-858A-8 Sequence 8, Appli
6	63	25.1	851	4	US-09-623-326-43 Sequence 43, Appli
7	62.5	24.9	1270	4	US-09-538-092-1321 Sequence 1321, Ap
8	61.5	24.5	309	4	US-09-248-786A-14974 Sequence 14974, A
9	61	24.3	442	3	US-09-081-689-2 Sequence 2, Appli
10	61	24.3	442	3	US-09-305-984-14 Sequence 14, Appli
11	61	24.3	442	3	US-09-073-541A-14 Sequence 14, Appli
12	61	24.3	442	4	US-09-493-940-14 Sequence 14, Appli
13	61	24.3	442	4	US-09-583-110-5317 Sequence 5317, Ap
14	61	24.3	446	4	US-09-107-433-3720 Sequence 3720, Ap
15	61	24.3	644	1	US-08-487-890A-6 Sequence 6, Appli
16	61	24.3	644	1	US-08-478-435-6 Sequence 6, Appli
17	61	24.3	644	2	US-08-337-483-6 Sequence 6, Appli
18	61	24.3	644	2	US-08-478-373-6 Sequence 6, Appli
19	61	24.3	644	3	US-08-478-671-6 Sequence 6, Appli
20	61	24.3	644	3	US-08-483-577A-6 Sequence 6, Appli
21	61	24.3	644	3	US-08-897-438-6 Sequence 6, Appli
22	61	24.3	644	3	US-08-637-654-6 Sequence 6, Appli
23	61	24.3	644	3	US-08-649-518-6 Sequence 6, Appli
24	60.5	24.1	87	3	US-09-284-033-3 Sequence 3, Appli
25	60.5	24.1	87	3	US-08-729-834B-3 Sequence 3, Appli
26	60.5	24.1	1217	4	US-09-949-016-7454 Sequence 7454, Ap
27	59.5	23.7	424	4	US-09-286-981B-14 Sequence 14, Appli

28	59.5	23.7	425	4	US-09-286-981B-13 Sequence 13, Appli
29	59.5	23.7	426	4	US-09-286-981B-12 Sequence 12, Appli
30	59.5	23.7	721	4	US-09-248-786A-18800 Sequence 18800, A
31	59	23.5	451	4	US-09-270-767-45139 Sequence 45139, A
32	59	23.5	2101	1	US-08-466-390-4 Sequence 4, Appli
33	59	23.5	2101	1	US-08-470-950-4 Sequence 4, Appli
34	59	23.5	2101	1	US-08-467-781-4 Sequence 4, Appli
35	59	23.5	2101	1	US-08-195-487-4 Sequence 4, Appli
36	59	23.5	2101	2	US-08-483-924-4 Sequence 4, Appli
37	59	23.5	2101	3	US-09-452-294-1 Sequence 1, Appli
38	59	23.5	2101	5	PCT-US93-06160-4 Sequence 4, Appli
39	59	23.5	2107	4	US-09-949-016-7646 Sequence 7646, Ap
40	59	23.5	2107	4	US-09-949-016-7647 Sequence 2, Appli
41	58.5	23.3	399	3	US-08-729-834B-2 Sequence 2, Appli
42	58.5	23.3	399	3	US-09-949-016-6466 Sequence 6466, Ap
43	58.5	23.3	404	4	US-09-949-016-8325 Sequence 8325, Ap
44	58.5	23.3	404	4	US-09-949-016-8325 Sequence 8, Appli
45	58	23.1	487	3	US-09-724-224-8

ALIGNMENTS

RESULT 1
US-09-270-767-43370
; Sequence 43370, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43370
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43370

Query Match 26.3%; Score 66; DB 4; Length 142;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 16; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

1 GVKETPOOKYQRLHEVQELTEVEKIKTKYK 32
Db 111 GVKETPOOKYQRLHEVQELTEVEKIKTKYK 142
US-09-902-540-14908
; Sequence 14908, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(11549)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14908
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14908
Query Match 25.7%; Score 64.5; DB 4; Length 639;

Best Local Similarity 31.9%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 12; Indels 9; Gaps 1;

Qy 1 GVKETPOQKQRLHVEQELTTEVEK-----IKTTVKESATEE 38
Db 151 GALBAVDEQYQOAIADVERLTSELEAASAEKDSIGLRTQLEALDEE 197

RESULT 3

US-09-513-999C-7806
Sequence 7806, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7806
LENGTH: 151
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -25...-1
OTHER INFORMATION: score 3.9
OTHER INFORMATION: seq RYGLILGGGVYV/SR
FEATURE:
NAME/KEY: UNSURE
LOCATION: 94
OTHER INFORMATION: Xaa=Ile or Lys or Asn or Arg or Ser or Thr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 103
OTHER INFORMATION: Xaa=Glu or Lys
US-09-513-999C-7806

Query Match 25.5%; Score 64; DB 4; Length 151;
Best Local Similarity 40.5%; Pred. No. 3;

Matches 17; Conservative 7; Mismatches 8; Indels 10; Gaps 1;

Qy 9 KYORLHVEQELTTEVEKIKTTVKESA-----TEEKL 40
Db 86 KYKRLKAEVKQSKLEKKETITTSARQKQKXIIEHQEKL 127

RESULT 4

US-09-107-532A-5587
Sequence 5587, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arindello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5587:

SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...193
SEQUENCE DESCRIPTION: SEQ ID NO: 5587:

US-09-107-532A-5587

Query Match 25.5%; Score 64; DB 4; Length 193;
Best Local Similarity 40.5%; Pred. No. 3.9;

Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

Qy 2 VKETPOQKQRLHVEQELTTEVEKIKTTVKESATEE 38
Db 70 VSEFVEQTVBELER--EPTAEIVVNETILEKTEE 104

RESULT 5

US-09-269-858A-8
Sequence 8, Application US/09269858A
Patent No. 6692932
GENERAL INFORMATION:
APPLICANT: Angerer, Bernhard
APPLICANT: Ankenbauer, Waltraud
APPLICANT: Boehringer, M.
APPLICANT: Bonch-Osmolovskaya, Elizaveta
APPLICANT: Markau, Ursula
APPLICANT: Reiser, Astrid
APPLICANT: Schmitz-Agheguyan, Gudrun
TITLE OF INVENTION: Thermostable DNA Polymerase from Anaerocellum Thermophilum
FILE REFERENCE: 4452
CURRENT APPLICATION NUMBER: US/09/269,858A
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: PCT/EP97/05390
PRIOR FILING DATE: 1996-10-03
PRIOR APPLICATION NUMBER: EP/96115877
PRIOR FILING DATE: 1996-10-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 850
TYPE: PRT
ORGANISM: Abedus herberti
US-09-269-858A-8

Query Match 25.1%; Score 63; DB 4; Length 850;
Best Local Similarity 30.9%; Pred. No. 28;
Matches 17; Conservative 15; Mismatches 19; Indels 4; Gaps 2;

QY 1 GVKETPOOKVORLHE---VOELTVEVKITVYKESATEERKLPVLAQAL 52
DB 192 GVKIGERKSAQKLEEYSSLEIYQNDIKRSIREKLEAGK-DMAFLSKRLATI 245

RESULT 6
US-09-623-326-43
; Sequence 43, Application US/09623326
; Patent No. 6607883
; GENERAL INFORMATION:
; APPLICANT: Frey et al.
; TITLE OF INVENTION: Polymerase Chimerae
; FILE REFERENCE: 4894
; CURRENT APPLICATION NUMBER: US/09/623,326
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: DE 198 10 879.6
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 851
; TYPE: PRT
; ORGANISM: Anaerocellum thermophilum
US-09-623-326-43

Query Match 25.1%; Score 63; DB 4; Length 851;
Best Local Similarity 30.9%; Pred. No. 28;
Matches 17; Conservative 15; Mismatches 19; Indels 4; Gaps 2;

QY 1 GVKETPOOKVORLHE---VOELTVEVKITVYKESATEERKLPVLAQAL 52
DB 192 GVKIGERKSAQKLEEYSSLEIYQNDIKRSIREKLEAGK-DMAFLSKRLATI 245

RESULT 7
US-09-538-092-1321
; Sequence 1321, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gluc, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 1321
; LENGTH: 1270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321

Query Match 24.9%; Score 62.5; DB 4; Length 1270;
Best Local Similarity 34.8%; Pred. No. 52;
Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 4 ETPOOKVORLHEVOELTVEVKITVYKESATEERKLPVLAQAL 49
DB 311 ESLQOVBALKERVDLTDLTIILKATIEKSGDAASVQL-KQL 355

RESULT 8
US-09-248-796A-14974
; Sequence 14974, Application US/09248796A

Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14974
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14974

Query Match 24.5%; Score 61.5; DB 4; Length 309;
Best Local Similarity 41.2%; Pred. No. 13;
Matches 14; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 3 KETPOQ---KQORLHEVOELTVEVKITVKE 33
DB 271 EETPIQDNPKRRIHBIIDTSDIEDIETPTPE 304

RESULT 9
US-09-081-689-2
; Sequence 2, Application US/09081689
; Patent No. 6165992
; GENERAL INFORMATION:
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Throup, John
; APPLICANT: Biswas, Sanjoy
; TITLE OF INVENTION: Histidine Kinase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechart, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,347
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GML0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 442 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-689-2

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Query Match Similarity    24.3%; Score 61; DB 3; Length 442;
Best Local Similarity     33.3%; Pred. No. 23;
Matches   18; Conservative      6; Mismatches   24; Indels       6; Gaps        19;

QY          2 VKETPQQKYORL-----LHEVOELTTEVEKIKTTVKESATEEKLTPVILAKOL 49
            :|||:|||:|||:::|||:|||||:|:|:|:|
Db          200 LKEQINSLYQHLLTVIADLHKNKAAILQLKKWKFVLNGASHSLKTPIASLKTL 253


RESULT 10
US-09-305-984-14
; Sequence 14, Application US/09305984B
; Patent No. 6331407
; GENERAL INFORMATION:
; APPLICANT: NO. 6331407ak, Rodger
; APPLICANT: Toumanen, Elaine
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016N1
; CURRENT APPLICATION NUMBER: US/09/305,984B
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: 60/084,399
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 09/305,984
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-305-984-14

Query Match           24.3%; Score 61; DB 3; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches   18; Conservative      6; Mismatches   24; Indels       6; Gaps        19;

QY          2 VKETPQQKYORL-----LHEVOELTTEVEKIKTTVKESATEEKLTPVILAKOL 49
            :|||:|||:|||:::|||:|||||:|:~::~|||
Db          200 LKEQINSLYQHLLTVIADLHKNKAAILQLKKWKFVLNGASHSLKTPIASLKTL 253


RESULT 11
US-09-073-541A-14
; Sequence 14, Application US/09073541A
; Patent No. 6448224
; GENERAL INFORMATION:
; APPLICANT: NO. 6448224ak, Rodger
; APPLICANT: Toumanen, Elaine
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016
; CURRENT APPLICATION NUMBER: US/09/073,541A
; CURRENT FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-073-541A-14

Query Match           24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches   18; Conservative      6; Mismatches   24; Indels       6; Gaps        19;

QY          2 VKETPQQKYORL-----LHEVOELTTEVEKIKTTVKESATEEKLTPVILAKOL 49
            :|||:|||:|||:::|||:|||||:|:~::~|||
Db          200 LKEQINSLYQHLLTVIADLHKNKAAILQLKKWKFVLNGASHSLKTPIASLKTL 253


RESULT 12
US-09-493-940-14
; Sequence 14, Application US/09493940

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; Patent No. 6630583
; GENERAL INFORMATION:
; APPLICANT: No. 6630583ak, Rodger
; APPLICANT: Toumanen, Etaline
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016N1
; CURRENT APPLICATION NUMBER: US/09/493,940
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/084,399
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 09/305,984
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-493-940-14

Query Match      24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred.No.23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

OY      2 VKETQOKYORL-----LHEVOELTTEVEKIKTTVESATEBEKLTPVLLAKOL 49
        :|||:|||:|||::|||:|||||:|||||:
Db       200 LKEQINSLYQHLLTVADIADHEKNREALQLERKMVFPLRGASHSLKTPLASLKIL 253

RESULT 13
US-09-583-110-5317
; Sequence 5317, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5317
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5317

Query Match      24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred.No.23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

OY      2 VKETQOKYORL-----LHEVOELTTEVEKIKTTVESATEBEKLTPVLLAKOL 49
        :|||:|||:|||::|||:|||||:|||||:
Db       200 LKEQINSLYQHLLTVADIADHEKNREALQLERKMVFPLRGASHSLKTPLASLKIL 253

RESULT 14
US-09-107-433-3720
; Sequence 3720, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Maitiam
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (8) LOCATION 1...446
SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
US-09-107-433-3720

Query March 24.3% Score 61; DB 4; Length 446;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

QY 2 VKETPOQKYQRL-----LHEVOELTTEVEKIKTTVKESATEBKLPVLAQOL 49
DB 204 LKEQINSIYQHLVYIADLHEKRAIILQLEKMYEFLRGASHELKTPLASIKIL 257

RESULT 15
US-08-487-890A-6
Sequence 6, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mirdin, Andrew
APPLICANT: Klein, Michael
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jdb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-6

Query March 24.3% Score 61; DB 1; Length 644;
Best Local Similarity 32.6%; Pred. No. 36;
Matches 15; Conservative 8; Mismatches 17; Indels 6; Gaps 1;

QY 2 VKETPOQKYQRLHEVOELTTEVE-----KIKTTVKESATEBKLT 41
DB 244 LRETDANKSQWRTKLYDLNDVHNSRFRGKVKPTKESSEHPT 289

Search completed: November 3, 2005, 22:05:57
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OW protein - protein search, using sw model

Run on: November 3, 2005, 21:53:15 ; Search time 93.7112 Seconds
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Title: 09782816-51

Perfect score: 251

Sequence: 1 GVKEETPOOKYORLLHEVDEL.....ESATEBKLPVLLAKQLAAL 52

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Database : Published Applications AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251	100.0	401	16 US-10-408-765A-1369	Sequence 1369, Ap
2	251	100.0	406	10 US-09-782-816A-53	Sequence 53, Appl
3	251	100.0	465	9 US-09-925-298-676	Sequence 676, Appl
4	251	100.0	465	14 US-10-102-806-676	Sequence 676, Appl
5	248	98.8	183	10 US-09-782-816A-54	Sequence 54, Appl
6	248	98.8	224	16 US-10-425-115-315831	Sequence 315831, Appl
7	246	98.0	52	10 US-09-782-816A-51	Sequence 51, Appl
8	231	92.0	134	14 US-10-106-698-6730	Sequence 6730, Appl
9	22	113	45.0	22 10 US-09-782-816A-3	Sequence 3, Appl
10	107	42.6	21	10 US-09-782-816A-4	Sequence 4, Appl
11	103	41.0	20	10 US-09-782-816A-5	Sequence 5, Appl

	12	103	41.0	23	10	US-09-782-816A-1	Sequence 1, Appl
	13	98	35.0	19	10	US-09-782-816A-6	Sequence 6, Appl
	14	93	37.1	18	10	US-09-782-816A-7	Sequence 7, Appl
	15	88	35.1	17	10	US-09-782-816A-8	Sequence 8, Appl
	16	81	32.3	16	10	US-09-782-816A-9	Sequence 9, Appl
	17	76	30.3	15	10	US-09-782-816A-10	Sequence 10, Appl
	18	72.5	28.9	53	10	US-09-782-816A-52	Sequence 52, Appl
	19	72.5	28.9	380	10	US-09-782-816A-56	Sequence 56, Appl
	20	72.5	28.9	380	20	US-11-097-143-4056	Sequence 4056, Appl
	21	71	28.3	14	10	US-09-782-816A-11	Sequence 11, Appl
	22	70.5	28.1	348	16	US-10-425-115-110465	Sequence 210465, A
	23	70.5	28.1	356	15	US-10-425-114-63356	Sequence 63356, A
	24	70	27.9	1087	20	US-11-097-143-22866	Sequence 22866, A
	25	70	27.9	1087	20	US-11-097-143-22869	Sequence 22869, A
	26	68	27.1	2368	9	US-09-815-242-5635	Sequence 5635, Ap
	27	68	27.1	2368	9	US-09-815-242-12389	Sequence 12389, A
	28	67	26.7	2478	9	US-09-815-242-5816	Sequence 5816, Ap
	29	67	26.7	2478	9	US-09-815-242-12967	Sequence 12967, A
	30	67	26.7	2478	17	US-10-470-0488-220	Sequence 220, App
	31	67	26.7	2481	15	US-10-282-122A-43762	Sequence 43762, A
	32	66	26.3	13	10	US-09-782-816A-12	Sequence 12, Appl
	33	66	26.3	386	15	US-10-282-122A-71967	Sequence 71967, A
	34	65.5	26.1	576	15	US-10-424-599-274041	Sequence 274041, A
	35	65.5	26.1	1837	15	US-10-369-493-22734	Sequence 22734, A
	36	64.5	25.7	348	16	US-10-437-963-139713	Sequence 139713, A
	37	64	25.5	185	16	US-10-842-740-3	Sequence 3, Appl
	38	64	25.5	188	10	US-09-284-320-12	Sequence 12, Appl
	39	64	25.5	188	14	US-10-028-072-2	Sequence 2, Appl
	40	64	25.5	188	14	US-10-140-808-2	Sequence 2, Appl
	41	64	25.5	188	14	US-10-121-049-2	Sequence 2, Appl
	42	64	25.5	188	14	US-10-123-904-2	Sequence 2, Appl
	43	64	25.5	188	14	US-10-140-470-2	Sequence 2, Appl
	44	64	25.5	188	14	US-10-175-746-2	Sequence 2, Appl
	45	64	25.5	188	14	US-10-176-918-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-408-765A-1369
Sequence 1369, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boi D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1369
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1369

Query Match 100.0%; Score 251; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 1, 5e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEETPOOKYORLLHEVDELTFVEVKITTVKESATEBKLPVLLAKQLAAL 52
Db 94 GVKEETPOOKYORLLHEVDELTFVEVKITTVKESATEBKLPVLLAKQLAAL 145

RESULT 2
US-09-782-816A-53
; Sequence 53, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: U0069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-816A-53

Query Match 100.0%; Score 251; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.6e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 52
DB 99 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 150

RESULT 3
US-09-925-298-676
; Sequence 676, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-676

Query Match 100.0%; Score 251; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 52
DB 158 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 209

RESULT 4
US-10-102-806-676

; Sequence 676, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-676

Query Match 100.0%; Score 251; DB 14; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 52
DB 158 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 209

RESULT 5
US-09-782-816A-54
; Sequence 54, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: U0069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-816A-54

Query Match 98.8%; Score 248; DB 10; Length 183;
Best Local Similarity 98.1%; Pred. No. 1.3e-19;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 52
DB 94 GVKETPOOKYORLHVEQELTTEVEKIKTTVKSATTEKLTPLYLAKQIAL 145

RESULT 6
US-10-425-115-315831


```
; Sequence 315831, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongmei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315831
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT457_51109C.1.pep
US-10-425-115-315831

Query Match          98.8%; Score 248; DB 16; Length 224;
Best Local Similarity 98.1%; Pred. No. 1.7e-19;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GVKETPOOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 52
Db 47 GVKETPOOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 98

RESULT 7
US-09-782-816A-51
; Sequence 51, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069,001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 44
; OTHER INFORMATION: Xaa = Val or Leu
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-51

Query Match          98.0%; Score 246; DB 10; Length 52;
Best Local Similarity 98.1%; Pred. No. 5e-20;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 GVKETPOOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 52
Db 1 GVKETPOOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 52

RESULT 8
US-10-106-698-6730
; Sequence 6730, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
```

```
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6730
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6730

Query Match          92.0%; Score 231; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.1e-18;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 TPQOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 52
Db 1 TPQOKYORLHVEOELTTEVEKIKTYVESATEBEKLTTPVLLAKQLAAL 48

RESULT 9
US-09-782-816A-3
; Sequence 3, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069,001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-3

Query Match          45.0%; Score 113; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GVKETPOOKYORLHVEOELT 22
Db 1 GVKETPOOKYORLHVEOELT 22

RESULT 10
US-09-782-816A-4
; Sequence 4, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
```

```
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-4
```

```
Query Match          42.6%; Score 107; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VKETPOOKYQRLHVEQELTT 22
         |||||
Db      1 VKETPOOKYQRLHVEQELTT 21
```

```
RESULT 11
US-09-782-816A-5
; Sequence 5, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-5
```

```
Query Match          41.0%; Score 103; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 KETPOOKYQRLHVEQELTT 22
         |||||
Db      1 KETPOOKYQRLHVEQELTT 20
```

```
RESULT 12
US-09-782-816A-1
; Sequence 1, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 23
```

```
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa = Val or Leu
; OTHER INFORMATION: The sequence is a Homo sapiens sequence when Xaa
; OTHER INFORMATION: represents Leu and a Mus musculus sequence when
; OTHER INFORMATION: Xaa represents Val.
US-09-782-816A-1
```

```
Query Match          41.0%; Score 103; DB 10; Length 23;
Best Local Similarity 95.7%; Pred. No. 0.00015;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      23 EVKIKTYVESATEKLTPLYL 45
         |||||
Db      1 EVKIKTYVESATEKLTPLYL 23
```

```
RESULT 13
US-09-782-816A-6
; Sequence 6, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-6
```

```
Query Match          39.0%; Score 98; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 ETPPOOKYQRLHVEQELTT 22
         |||||
Db      1 ETPPOOKYQRLHVEQELTT 19
```

```
RESULT 14
US-09-782-816A-7
; Sequence 7, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
```

OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-7

Query Match 37.1%; Score 93; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPQKQRLHVEVQELTT 22
|||||
Db 1 TPQKQRLHVEVQELTT 18

RESULT 15
US-09-782-816A-8
Sequence 8, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:

APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069, 001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 17
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-8

Query Match 35.1%; Score 88; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQCKYQRLHVEVQELTT 22
|||||
Db 1 PQCKYQRLHVEVQELTT 17

Search completed: November 3, 2005, 22:11:40
Job time : 93.7112 secs

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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:32:33 ; Search time 72.5562 Seconds
(without alignments)
282.516 Million cell updates/sec

Title: 09782816-52

Sequence: 1 GKRTPYQKCRLOIEMNEL.....ADERSQSDAVATVISTAR 53

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19908:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	53	5	ABP53017 Cellular
2	243.5	94.4	380	4	ABP53017 Cellular
3	243.5	94.4	380	5	ABP53020 Drosophila
4	114	44.2	22	5	ABP52991 Cellular
5	108	41.9	21	5	ABP52992 Cellular
6	105	40.7	22	5	ABP52992 Cellular
7	103	39.9	20	5	ABP52993 Cellular
8	98	38.0	19	5	ABP52994 Cellular
9	93	36.0	18	5	ABP52995 Cellular
10	88	34.1	17	5	ABP52996 Cellular
11	81	31.4	16	5	ABP52997 Cellular
12	77	29.8	15	5	ABP52998 Cellular
13	74	28.7	183	5	ABP53019 Cellular
14	72.5	28.1	52	5	ABP53016 Cellular
15	72.5	28.1	314	6	ABP53016 Cellular
16	72.5	28.1	378	6	ABP53016 Cellular
17	72.5	28.1	401	7	ABP53016 Cellular
18	72.5	28.1	401	7	ABP53016 Cellular
19	72.5	28.1	465	5	ABP53016 Cellular
20	72.5	27.3	14	5	ABP52999 Cellular
21	70.5	27.3	1937	8	ADQ17289 Human sof
22	70.5	27.3	1937	8	ADQ17242 Human sof
23	69.5	26.9	97	4	ABP38174 Peptide #
24	69.5	26.9	97	4	ABP38174 Peptide #
25	69.5	26.9	97	4	ABP38174 Peptide #

26	69.5	26.9	97	4	AA558807 Human bra
27	69.5	26.9	97	4	ABG53031 Human liv
28	69.5	26.9	97	5	ABG41126 Human pep
29	67	26.0	13	5	ABP53000 Cellular
30	62.5	24.2	97	4	AA119334 Peptide #
31	62.5	24.2	97	4	ABP38669 Peptide #
32	62.5	24.2	97	4	AA132130 Peptide #
33	62.5	24.2	97	4	ABP23745 Protein #
34	62.5	24.2	97	4	AA171845 Human don
35	62.5	24.2	97	4	AA159298 Human bra
36	62.5	24.2	97	4	ABG53529 Human liv
37	62.5	24.2	97	5	ABG41658 Human pep
38	62.5	24.2	103	4	ABP26895 Protein #
39	62.5	24.2	103	4	AA177111 Human don
40	62.5	24.2	892	7	ABP79862 Rat myosi
41	62.5	24.2	892	7	ABP47859 Rat prote
42	62.5	24.2	892	7	ABP47855 Rat prote
43	62.5	24.2	1939	7	ABP47857 Human pro
44	62.5	24.2	1939	7	ABP47861 Human pro
45	62.5	24.2	1939	7	ABP47033 Human pro

ALIGNMENTS

RESULT 1	ABP53017	ABP53017 standard; peptide; 53 AA.
XX	AC	ABP53017;
DT	05-NOV-2002	(first entry)
XX	XX	Cellular proliferation peptide inhibitor SEQ ID NO:52.
XX	XX	Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytic disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoele disorder; angiogenic disorder; immunologic disorder.
XX	OS	Drosophila melanogaster.
XX	XX	WO200264779-A2.
PD	22-AUG-2002.	
XX	XX	21-JAN-2002; 2002WO-US001708.
PF	XX	14-FEB-2001; 2001US-00782816.
PR	XX	(REGC) UNIV CALIFORNIA.
PA	XX	Sharp DJ, Rogers GC, Scholey JW; WPI, 2002-657599/70.
P1	XX	New peptide inhibitors of p50/dynamin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
PT	XX	Claim 3; Page 31; 55pp; English.
PT	XX	The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytosolic and antiinflammatory activities and can be used as p50/dynamin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such

CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoealic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a specifically claimed peptide inhibitor of cellular
CC proliferation from the present invention

XX
SQ Sequence 53 AA;

Query Match 100.0%; Score 258; DB 5; Length 53;

Best Local Similarity 100.0%; Pred. No. 2.4e-26; Mismatches 0; Indels 0; Gaps 0;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKEETPVQKCORLQIEMNELINEVAALQVDRKVADEEKQSYDAVAVTISTAR 53
DB 1 GKEETPVQKCORLQIEMNELINEVAALQVDRKVADEEKQSYDAVAVTISTAR 53

RESULT 2

ABBS9088 ID ABBS9088 standard; protein; 380 AA.

XX
AC ABBS9088;

XX
DT 26-MAR-2002 (first entry)

XX
DE Drosophila melanogaster polypeptide SEQ ID NO 4056.

XX
KW Drosophila; developmental biology; cell signalling; insecticide;

XX
KW pharmaceutical.

XX
OS Drosophila melanogaster.

XX
PN WO200171042-A2.

XX
XX 27-SEP-2001.

XX
PP 23-MAR-2001; 2001WO-US0009231.

XX
PR 23-MAR-2000; 2000US-0191637P.

XX
PR 11-JUL-2000; 2000US-00614150.

XX
PA (PEKE) PE CORP NY.

XX
PI Venter JC, Adams M, Li PWD, Myers EW;

XX
DR WPI; 2001-656860/75.

XX
DR N-PSDB; ABL03191.

XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.

XX
PS Disclosure: SEQ ID NO 4056; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signaling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX ABBS72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 380 AA;

Query Match 94.4%; Score 243.5; DB 4; Length 380;

Best Local Similarity 98.1%; Pred. No. 2.4e-23;

Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GKEETPVQKCORLQIEMNELINEVAALQVDRKVADEEKQSYDAVAVTISTAR 53
DB 94 GKEETPVQKCORLQIEMNELINEVAALQVDRKVADEEKQSYDAVAVTISTAR 145

RESULT 3

ABPS3020 ID ABPS3020 standard; protein; 380 AA.

XX
AC ABPS3020;

XX
DT 05-NOV-2002 (first entry)

XX
DE Drosophila melanogaster p50 protein sequence SEQ ID NO:56.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
XX p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
XX sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
XX glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
XX glandular disorder; macrophagal disorder; epithelial disorder;
XX stromal disorder; blastocoealic disorder; angiogenic disorder;
XX immunologic disorder; p50.

XX
OS Drosophila melanogaster.

XX
PN WO200264779-A2.

XX
PD 22-AUG-2002.

XX
PE 21-JAN-2002; 2002WO-US001708.

XX
PR 14-FEB-2001; 2001US-00782816.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Sharp DJ, Rogers GC, Scholey JW;

XX
DR WPI; 2002-657599/70.

XX
DR N-PSDB; ABQ75378.

XX
PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.

XX
PS Example 1; Fig 4; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABPS2966 and ABPS2967 and can have C-terminal and N-
XX terminal extensions. (I) have cytosstatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumours (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumours); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoealic disorders; and
XX inflammatory, angiogenic and immunologic disorders. The present sequence
XX represents Drosophila melanogaster p50 which is given in the
XX exemplification of the present invention

SQ Sequence 380 AA;

Query Match 94.4%; Score 243.5; DB 5; Length 380;

Best Local Similarity 98.1%; Pred. No. 2.4e-23; Mismatches 0; Indels 1; Gaps 1;

QY 1 GKEETPVQKCORLQIEMNELINEVAALQVDRKVADEEKQSYDAVAVTISTAR 53

Db 94 GSEKTPVOKCQRLQIEMNELINVAALQVDRKVADEEKSYDA-VAIVISTAR 145.

RESULT 4

ABP52991 ID ABP52991 standard; peptide: 22 AA.

AC ABP52991;

DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:26.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
 KW glandular disorder; macrophagal disorder; epithelial disorder;
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
 KW immunologic disorder.

OS Drosophila melanogaster.

PN WO200264779-A2.

PD 22-AUG-2002.

PE 21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

PA (REGC) UNIV CALIFORNIA.

PI Sharp DJ, Rogers GC, Scholey JM;

PT WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.

XX Claim 1; Page 30; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
 CC inflammatory, angiogenic and immunologic disorders. The present sequence
 CC represents a peptide that can be N-terminally added to (P2)

XX Sequence 22 AA;

Query Match 44.2%; Score 114; DB 5; Length 22;

Best Local Similarity 100.0%; Pred. No. 8e-08; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSEKTPVOKCQRLQIEMNELIN 22

Db 1 GSEKTPVOKCQRLQIEMNELIN 22

RESULT 5

ABP52992 ID ABP52992 standard; peptide: 21 AA.

AC ABP52992;

DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:27.

XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
 KW glandular disorder; macrophagal disorder; epithelial disorder;
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
 KW immunologic disorder.

OS Drosophila melanogaster.

PN WO200264779-A2.

PD 22-AUG-2002.

PE 21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

PA (REGC) UNIV CALIFORNIA.

PI Sharp DJ, Rogers GC, Scholey JM;

PT WPI; 2002-657599/70.

XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.

XX Claim 1; Page 30; 55pp; English.

XX The present invention describes an isolated peptide (I) comprising or
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (I) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
 CC inflammatory, angiogenic and immunologic disorders. The present sequence
 CC represents a peptide that can be N-terminally added to (P2)

XX Sequence 21 AA;

Query Match 41.9%; Score 108; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.7e-07; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKETPVOKCQRLQIEMNELIN 22

Db 1 EKETPVOKCQRLQIEMNELIN 21

RESULT 6

ABP52967 ID ABP52967 standard; peptide: 22 AA.

AC ABP52967;

DT 05-NOV-2002 (first entry)
 XX Cellular proliferation inhibitor related peptide SEQ ID NO:2.
 XX
 XX Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
 KW glandular disorder; macropagal disorder; epithelial disorder;
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
 KW immunologic disorder.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200264779-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX 21-JAN-2002; 2002WO-US001708.
 PF
 XX 14-FEB-2001; 2001US-00782816.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Sharp DJ, Rogers GC, Scholey JM;
 PI
 XX MPI, 2002-657599/70.
 DR
 XX
 XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.
 PT
 XX Claim 1; Page 29; 55pp; English.
 PS
 XX The present invention describes an isolated peptide (1) comprising or
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macropagal, epithelial, stromal and blastocoeleic disorders; and
 CC inflammatory, angiogenic and immunologic disorders
 CC
 XX Sequence 22 AA;
 SQ
 Query Match 40.7%; Score 105; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 EVAALQVDRKVADEKQSYDAY 44
 DB 1 EVAALQVDRKVADEKQSYDAY 22
 RESULT 7
 ABP52993
 ID ABP52993 standard; peptide; 20 AA.
 AC ABP52993;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 XX Cellular proliferation inhibitor related peptide SEQ ID NO:28.
 DE
 KW Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW immunologic disorder.

KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
 KW glandular disorder; macropagal disorder; epithelial disorder;
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
 KW immunologic disorder.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200264779-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX 21-JAN-2002; 2002WO-US001708.
 PF
 XX 14-FEB-2001; 2001US-00782816.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Sharp DJ, Rogers GC, Scholey JM;
 PI
 XX MPI, 2002-657599/70.
 DR
 XX
 XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.
 PT
 XX Claim 1; Page 30; 55pp; English.
 PS
 XX The present invention describes an isolated peptide (1) comprising or
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macropagal, epithelial, stromal and blastocoeleic disorders; and
 CC inflammatory, angiogenic and immunologic disorders. The present sequence
 CC represents a peptide that can be N-terminally added to (P2)
 CC
 XX Sequence 20 AA;
 SQ
 Query Match 39.9%; Score 103; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 2e-06;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KETPVOKCQRLQIEMNELLN 22
 DB 1 KETPVOKCQRLQIEMNELLN 20
 RESULT 8
 ABP52994
 ID ABP52994 standard; peptide; 19 AA.
 AC ABP52994;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 XX Cellular proliferation inhibitor related peptide SEQ ID NO:29.
 DE
 KW Cellular proliferation inhibitor; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
 KW glandular disorder; macropagal disorder; epithelial disorder;
 KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
 KW immunologic disorder.

XX OS Drosophila melanogaster.
XX PN WO200264779-A2.
XX PD 22-AUG-2002.
XX PF 21-JAN-2002; 2002WO-US001708.
XX PR 14-FEB-2001; 2001US-00782816.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Sharp DJ, Rogers GC, Scholey JM;
XX DR WPI; 2002-657599/70.
XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX PT immunologic disorders.
XX PS Claim 1; Page 30; 55pp; English.
XX CC The present invention describes an isolated peptide (1) comprising or
XX CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX CC terminal extensions. (1) have cytosstatic and antiinflammatory activities
XX CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX CC peptides, nucleic acid molecules and methods from the present invention
XX CC are useful for treating cancer by inhibiting cellular proliferation, such
XX CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX CC neck tumors); leukemias and lymphoid malignancies, other disorders such
XX CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
XX CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
XX CC inflammatory, angiogenic and immunologic disorders. The present sequence
XX CC represents a peptide that can be N-terminally added to (P2)
XX SO Sequence 19 AA;
QY Query Match 38.0%; Score 98; DB 5; Length 19;
Db Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ETPVOKCQRLQIEMNELIN 22
Db 1 ETPVOKCQRLQIEMNELIN 19
RESULT 9
ABP52995
ID ABP52995 standard; peptide; 18 AA.
XX AC ABP52995;
XX DT 05-NOV-2002 (first entry)
XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:30.
XX KW Cellular proliferation inhibition; cytosstatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.
XX OS Drosophila melanogaster.
XX PN WO200264779-A2.

PD 22-AUG-2002.
XX PF 21-JAN-2002; 2002WO-US001708.
XX PR 14-FEB-2001; 2001US-00782816.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Sharp DJ, Rogers GC, Scholey JM;
XX DR WPI; 2002-657599/70.
XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX PT immunologic disorders.
XX PS Claim 1; Page 30; 55pp; English.
XX CC The present invention describes an isolated peptide (1) comprising or
XX CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX CC terminal extensions. (1) have cytosstatic and antiinflammatory activities
XX CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX CC peptides, nucleic acid molecules and methods from the present invention
XX CC are useful for treating cancer by inhibiting cellular proliferation, such
XX CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX CC neck tumors); leukemias and lymphoid malignancies, other disorders such
XX CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
XX CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
XX CC inflammatory, angiogenic and immunologic disorders. The present sequence
XX CC represents a peptide that can be N-terminally added to (P2)
XX SO Sequence 18 AA;
QY Query Match 36.0%; Score 93; DB 5; Length 18;
Db Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TPVOKCQRLQIEMNELIN 22
Db 1 TPVOKCQRLQIEMNELIN 18
RESULT 10
ABP52996
ID ABP52996 standard; peptide; 17 AA.
XX AC ABP52996;
XX DT 05-NOV-2002 (first entry)
XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:31.
XX KW Cellular proliferation inhibition; cytosstatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.
XX OS Drosophila melanogaster.
XX PN WO200264779-A2.
XX PD 22-AUG-2002.
XX PF 21-JAN-2002; 2002WO-US001708.
XX PR 14-FEB-2001; 2001US-00782816.

XX (REGC) UNIV CALIFORNIA.
PA Sharp DJ, Rogers GC, Scholey JM;
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.
XX
XX Claim 1; Page 30; 55pp; English.
XX
XX The present invention describes an isolated peptide (1) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P2)
XX
SQ Sequence 17 AA;
XX
Query Match 34.1%; Score 88; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 PVQKCRQLQIEMNELLN 22
Db 1 PVQKCRQLQIEMNELLN 17
XX
RESULT 11
ABP52997
ID ABP52997 standard; peptide; 16 AA.
XX
AC ABP52997;
XX
DT 05-NOV-2002 (first entry)
XX
DE Cellular proliferation inhibitor related peptide SEQ ID NO:32.
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200264779-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 21-JAN-2002; 2002WO-US001708.
PF
XX
XX 14-FEB-2001; 2001US-00782816.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA Sharp DJ, Rogers GC, Scholey JM;
XX
XX
XX

DR WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.
XX
XX Claim 1; Page 30; 55pp; English.
XX
XX The present invention describes an isolated peptide (1) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P2)
XX
SQ Sequence 16 AA;
XX
Query Match 31.4%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7 VQKCRQLQIEMNELLN 22
Db 1 VQKCRQLQIEMNELLN 16
XX
RESULT 12
ABP52998
ID ABP52998 standard; peptide; 15 AA.
XX
XX
AC ABP52998;
XX
DT 05-NOV-2002 (first entry)
XX
DE Cellular proliferation inhibitor related peptide SEQ ID NO:33.
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200264779-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 21-JAN-2002; 2002WO-US001708.
PF
XX
XX 14-FEB-2001; 2001US-00782816.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA Sharp DJ, Rogers GC, Scholey JM;
XX
XX
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and

PT immunologic disorders.
 XX
 PS Claim 1, Page 30, 55pp; English.
 XX
 CC The present invention describes an isolated peptide (I) comprising or
 CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
 CC macrophagal, epithelial, stromal and blastocoele disorders; and
 CC inflammatory, angiogenic and immunologic disorders. The present sequence
 CC represents a peptide that can be N-terminally added to (P2)
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 29.8%; Score 77; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 QKCRQLQIEMNELIN 22
 |||||
 1 QKCRQLQIEMNELIN 15
 DB
 RESULT 13
 ABP53019
 ID ABP53019 standard; protein; 183 AA.
 XX
 AC ABP53019;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Mouse p50 amino acid sequence SEQ ID NO:54.
 XX
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
 KW glandular disorder; macrophagal disorder; epithelial disorder;
 KW stromal disorder; blastocoele disorder; angiogenic disorder;
 KW immunologic disorder.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 XX
 PN WO200264779-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 21-JAN-2002; 2002WO-US001708.
 XX
 PR 14-FEB-2001; 2001US-00782816.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Sharp DJ, Rogers GC, Scholey JM,
 DR WPI; 2002-657599/70.
 XX
 PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.
 XX
 PS Disclosure; Fig 2; 55pp; English.
 XX
 CC The present invention describes an isolated peptide (I) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
 CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
 CC terminal extensions. (1) have cytostatic and antiinflammatory activities
 CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
 CC peptides, nucleic acid molecules and methods from the present invention
 CC are useful for treating cancer by inhibiting cellular proliferation, such
 CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
 CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
 CC neck tumors); leukemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytal, hypochalamic and other glandular,
 CC macrophagal, epithelial, stromal and blastocoele disorders; and
 CC inflammatory, angiogenic and immunologic disorders. The present sequence
 CC represents mouse p50 which is given in the exemplification of the present
 CC invention
 CC
 XX
 SQ Sequence 183 AA;
 Query Match 28.7%; Score 74; DB 5; Length 183;
 Best Local Similarity 35.8%; Pred. No. 0.23;
 Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
 Oy 1 GKEETPVQKCRQLQIEMNELINEVALQVDRKVADEEKOSYDAVATVISTAR 53
 |||||
 94 GVKETPQOKTQRLHVEVQELTTEVEKIKTYKESATREKTLPPVLAQQLALK 146
 DB
 RESULT 14
 ABP53016
 ID ABP53016 standard; peptide; 52 AA.
 XX
 AC ABP53016;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Cellular proliferation peptide inhibitor SEQ ID NO:51.
 XX
 KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
 KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
 KW sarcoma; glioblastoma; leukaemia; lymphoid malignancy; neuronal disorder;
 KW glial disorder; astrocytal disorder; hypochalamic disorder; inflammatory;
 KW glandular disorder; macrophagal disorder; epithelial disorder;
 KW stromal disorder; blastocoele disorder; angiogenic disorder;
 KW immunologic disorder.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 44
 FT /label= 'Leu, Val
 FT /note= "Leu in humans and Val in Mus musculus"
 XX
 PN WO200264779-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 21-JAN-2002; 2002WO-US001708.
 XX
 PR 14-FEB-2001; 2001US-00782816.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Sharp DJ, Rogers GC, Scholey JM,
 DR WPI; 2002-657599/70.
 XX
 PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
 PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
 PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
 PT immunologic disorders.
 XX

PS Claim 2; Page 31; 55pp; English.

The present invention describes an isolated peptide (1) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP5267 and can have C-terminal and N-terminal extensions. (1) have cytotoxic and antiinflammatory activities and can be used as p50/dynamin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumors (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumors); leukemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoele disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a specifically claimed peptide inhibitor of cellular proliferation from the present invention

SQ Sequence 52 AA;

Query Match	28.1%;	Score	72.5;	DB	5;	Length	52;
Best Local Similarity	48.7%;	Pred. No.	0.072;				
Matches	19;	Conservative	5;	Mismatches	14;	Indels	1;
						Gaps	1;

QY 1 GEKETPVQCCQRLQIEMNELNEVALQVD-RKVADDEEK 38
| | | | | : | | : : | | |
1 GVKETPVQCKQRLNHEVQELTTEVEKIKITTVKESATEEK 39

RESULT 15
ABM81421

ID ABM81421 standard; protein; 314 AA.

AC ABM81421;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.

KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytosstatic.

OS Homo sapiens.

PN WO2004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

DR WPI; 2004-347921/32.

DR N-PSDB; ACN3

PT New tumor-associated antigenic target polypeptides and nucleic acids
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

PS Claim 12; SEQ ID NO 3675; 7273bp; English

CC The invention relates to human tumour-associated antigenic target (TAT)

polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

Sequence 314 AA;

Query Match	28.1%	Score	72.5	DB	8	Length	314
Best Local Similarity	48.7%	Pred. No.	0.71				
Matches	19	Conservative	5	Mismatches	14	Indels	1
						Gaps	1

QY 1 GEKETPVOKCÖRQLÖIEMNELNEVAALÖVD-RKVADEEK 38
| | | | | : | | | : : | | |
7 GYKETPÖÖKYÖRLLHEVÖELTTEVEKIKTTVESATBEK 45

Search completed: November 3, 2005, 21:57:31
Job time : 73.5562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 19.2727 Seconds

(without alignments)
264.596 Million cell updates/sec

Title: 09782816-52

Sequence: 1 GKEKTPYQKCRQLQIEMNEL.....ADEEKQSYDAVAVTISTAR 53

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70.5	27.3	1937	2	I38055 myosin heavy chain
2	69.5	26.9	230	2	AC1523 hypothetical prote
3	68	26.4	297	2	H72670 hypothetical prote
4	67.5	26.2	162	2	H70314 hypothetical prote
5	66	25.6	508	2	G84739 hypothetical prote
6	65	25.2	730	2	T38346 hypothetical prote
7	64.5	25.0	157	2	B81688 conserved hypotnat
8	63.5	24.6	676	2	S00084 myosin heavy chain
9	63.5	24.6	698	2	S52696 myosin heavy chain
10	63.5	24.6	1938	1	UX0178 myosin heavy chain
11	63	24.4	111	2	F64596 myosin heavy chain
12	62.5	24.2	222	2	E84283 TRK potcaasium upta
13	62.5	24.2	955	2	S24348 myosin heavy chain
14	62.5	24.2	1938	2	A59293 skeletal myosin he
15	62	24.0	230	2	AC1164 hypothetical prote
16	62	24.0	596	2	H81095 conserved hypotnat
17	62	24.0	601	2	F81846 hypothetical sece
18	62	24.0	743	2	D84854 hypothetical prote
19	62	24.0	1133	2	T22976 hypothetical prote
20	60.5	23.4	900	2	T33482 hypothetical prote
21	60	23.3	1050	2	A89769 hypothetical prote
22	59.5	23.1	1050	2	A59088 ABC transporter -
23	59.5	23.1	741	2	S39082 myosin heavy chain
24	59.5	23.1	936	2	S39083 myosin heavy chain
25	59.5	23.1	1940	1	S04090 myosin heavy chain
26	59	22.9	110	2	H71915 phosphoglycerate m
27	58.5	22.7	503	2	A82831 N utilization subs
28	58.5	22.7	503	2	A82831 myosin heavy chain
29	58.5	22.7	1940	1	A24922

30	58	22.5	223	2	P00514 hemagglutinin HA2
31	58	22.5	412	2	S07537 myosin heavy chain
32	58	22.5	463	2	G97884 argininosuccinate
33	58	22.5	621	2	S10450 myosin heavy chain
34	58	22.5	650	2	T00617 endosyle-specific
35	58	22.5	866	2	S04027 paramyosin - Caeno
36	58	22.5	872	2	T19296 hypothetical prote
37	58	22.5	1255	2	T31065 diaphanous protein
38	58	22.5	2297	2	AB2494 hypothetical prote
39	57.5	22.3	271	2	A30592 33k cytoskeletal p
40	57.5	22.3	272	1	SJG086 giardin beta chain
41	57.5	22.3	410	2	H95888 hypothetical prote
42	57.5	22.3	560	2	S53382 protein YKR029c ho
43	57.5	22.3	629	2	T34370 hypothetical prote
44	57.5	22.3	791	2	T27473 hypothetical prote
45	57.5	22.3	876	2	A23767 myosin heavy chain

ALIGNMENTS

RESULT 1
I38055
myosin heavy chain, perinatal skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
C/Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R:Jullian, B.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Steadman, H.H.
Burr, J. Biochem. 230, 1001-1006, 1995
A>Title: Characterization of a human perinatal myosin heavy-chain transcript.
A/Reference number: I38055; MUID:95324556; PMID:7601129
A/Accession: I38055
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1937 <RES>
A/Cross-references: UNIPROT:P13535; EMBL:Z38133; NID:G558668; PIDN:CA86293.1; PID:G5586
R:Karsch-Mizrachi, I.; Peghali, R.; Shows, T.B.; Leinwand, L.A.
Gene 89, 289-294, 1990
A>Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.
A/Reference number: JH0154; MUID:90323631; PMID:2373371
A/Accession: JH0154
A/Molecule type: mRNA
A/Residues: 1-14, 'A', 16-85 <KAR>
A/Cross-references: GB:Y00821
A/Experimental source: skeletal muscle
R:Bober, E.
submitted to the EMBL Data Library, January 1989
A/Reference number: S12458
A/Accession: S12459
A/Molecule type: mRNA
A/Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>
A/Cross-references: EMBL:X51592; NID:929465; PIDN:CA83941.1; PID:G29466
A/Experimental source: clone gEMC-F
R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A>Title: Identification of three developmentally controlled isoforms of human myosin hea
A/Reference number: S09331; MUID:90235862; PMID:1691980
A/Accession: S09332
A/Molecule type: mRNA
A/Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 899-
1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668-17
A/Cross-references: EMBL:X51592
R:Peghali, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A>Title: Molecular genetic characterization of a developmentally regulated human perinat
A/Reference number: A30220; MUID:89234168; PMID:2715175
A/Accession: A30220
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-184
A/Cross-references: GB:Y00821; NID:G34863; PIDN:CA68757.1; PID:G34864
C/Genetic: B

A:Gene: GDB:MYH8
A:Cross-references: GDB:125267; OMIM:160741
A:Map position: 17pter-17p12
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F:91-769/Domain: myosin motor domain homology <MMOT>
F:181-168/Region: nucleotide-binding motif A (P-loop)
F:551-588/Region: actin binding #status predicted
F:658-680/Region: actin binding #status predicted
F:847-1282/Region: S2 #status predicted
F:698,708/Active site: Cys #status predicted

Query Match 27.3%; Score 70.5; DB 2; Length 1937;
Best Local Similarity 28.9%; Pred. No. 12;
Matches 22; Conservative 15; Mismatches 8; Indels 31; Gaps 4;

Oy 2 EKETPVQKQ-----RLQIEMNELNEVALQVDRKVA--DEE-- 37
Db 1533 KKQVEQKCEIQALERAEASLEHBEKILRIQLINQVSE----VDRKIAEKDESID 1587

Oy 38 --KOSYDAVVATVIST 51
Db 1568 QLKRNHTRVETMOST 1603

RESULT 2
AC1523
hypothetical protein lin0723 [imported] - *Listeria innocua* (strain C1p11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1523
R:Glaser, P.; Fraigneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entlian, K.D.; Fehli, H.
D.; Jones, L.M.; Karsc, U.
Science 294, 849-852, 2001
A:Authors: Kreitt, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <GLA>
A:Cross-references: UNIPROT:Q92PT9; GB:AL592022; PIDN:GAC95955.1; PID:g16413175; GSPDB:G
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin0723

Query Match 26.9%; Score 69.5; DB 2; Length 230;
Best Local Similarity 30.5%; Pred. No. 1.6;
Matches 18; Conservative 10; Mismatches 16; Indels 15; Gaps 1;

Oy 2 EKETPVQK-----CRLQIEMNELNEVALQVDRKVADEEKSYDAVV 45
Db 33 EVESYSEKLEQLLENHQKLEKMSAIEIQOKLANEKAAALKAERQALIEIKQSAEAI 91

RESULT 3
H72670
hypothetical protein APE0790 - *Aeropyrum pernix* (strain K1)
C:Species: *Aeropyrum pernix*
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72670
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr*
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:Q9YDX9; DBJ:AP000060; NID:g5104188; PIDN:BAA79768.1; PID:d1

A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0790

Query Match 26.4%; Score 68; DB 2; Length 297;
Best Local Similarity 46.7%; Pred. No. 3.1;
Matches 14; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 12 RLQIEMNELNEVALQVDRKVADEEKSY 41
Db 29 RLKEERKLNEVALNEERKASREKREY 58

RESULT 4
H70314
hypothetical protein aq_157 - *Aquifex aeolicus*
C:Species: *Aquifex aeolicus*
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: H70314
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
v.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: H70314
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <AGP>
A:Cross-references: UNIPROT:O66547; GB:AE000676; NID:g2982884; PIDN:AAC06512.1; PID:g298:
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_157

Query Match 26.2%; Score 67.5; DB 2; Length 162;
Best Local Similarity 35.3%; Pred. No. 1.9;
Matches 18; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Oy 3 KETPVQKQRLQIEMNELNEVALQVDRKVADEEKSYDAVVATVISTAR 53
Db 81 KEKAKAIEIQLEDBRLKIQVE-AQSKSRKKAIEKXVPKVIKIVESTAK 130

RESULT 5
C84799
hypothetical protein At2g37960 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84799
R:Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; J
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanbaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84799
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <STO>
A:Cross-references: UNIPROT:Q7XJQ8; GB:AE002093; NID:g4895188; PIDN:AA032775.1; GSPDB:GNI
A:Gene: At2g37960
A:Map position: 2

Query Match 25.6%; Score 66; DB 2; Length 508;
Best Local Similarity 34.2%; Pred. No. 9.1;
Matches 13; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Oy 5 TPVQKQRLQIEMNELNEVALQVDRKVADEEKSYD 42
Db 55 SPAREVNSLPLINEIINEYIRLKKKIVMDQESKID 92

RESULT 6

T38346
 hypotheoretical protein SPAC24C9.05c - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T38346
 R/Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1995
 A/Reference number: Z21787
 A/Accession: T38346
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-730 <MDS>
 A/Cross-references: UNIPROT:O13965; EMBL:Z98601; PDB:1CAB1262.1; GSPDB:GN00066; SPDB:SF
 A/Experimental source: strain 972h-; cosmid c24C9
 C/Genetics:
 A/Gene: SPDB:SPAC24C9.05c
 A/Map position: 1

Query Match 25.2%; Score 65; DB 2; Length 730;
 Best Local Similarity 28.2%; Pred. No. 17;
 Matches 20; Conservative 11; Mismatches 20; Indels 20; Gaps 2;

Qy 1 GKEETPVQKCORLQIEMNELNEVAALQVDRKVA--VADEEKOS 40
 Db 47 GNFSPVARKIRNGEPGTVDNALDPALTYMOSLIVETRAQLMAKRONCVLVDDDEQL 106

Qy 41 YDAVVAIVTIST 51
 Db 107 AGIVATDIAT 117

RESULT 7
 B81688
 conserved hypotheoretical protein TC0569 [imported] - Chlamydia muridarum (strain Nig9)
 C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: B81688
 R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A/Reference number: A81500; MUID:20150255; PMID:10684935
 A/Accession: B81688
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-157 <TEP>
 A/Cross-references: UNIPROT:Q9PK98; GB:AE002325; GB:AE002160; NID:G7190604; PIDN:AAF3940
 A/Experimental source: strain Nig9 (MoPn)
 C/Genetics:
 A/Gene: TC0569

Query Match 25.0%; Score 64.5; DB 2; Length 157;
 Best Local Similarity 31.5%; Pred. No. 3.9;
 Matches 17; Conservative 12; Mismatches 22; Indels 3; Gaps 2;

Qy 2 EKETPVQKCORLQIEMNELNEVAALQVDRKVADEKOSYDAV--VATVISTAR 53
 Db 24 EKIPVSPCKIKELAKQFLKEVAVAK-DRYLQKRENNVYSLPGVAIVKAR 76

RESULT 8
 S00084
 myosin heavy chain, fast skeletal muscle - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: S00084; S14807
 R/Maeda, K.; Szekiel, G.; Wittlinghofer, A.
 Eur. J. Biochem. 167, 97-102, 1987
 A/Title: Characterization of cDNA coding for the complete light meromyosin portion of a
 A/Reference number: S00084; MUID:87304245; PMID:3305014
 A/Accession: S00084
 A/Molecule type: mRNA
 A/Residues: 1-676 <MAE>

A/Cross-references: UNIPROT:P02562; EMBL:X05958; NID:G1622; PIDN:CAA29391.1; PID:G136424
 A/Note: the sequence from Fig. 5 is inconsistent with that from Fig. 3 in having 561-Arg
 R/Maeda, K.; Roesch, A.; Maeda, Y.; Kalbitzer, H.R.; Wittlinghofer, A.
 FEBS Lett. 281, 23-26, 1991
 A/Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its role in molec
 A/Reference number: S14807; MUID:91200294; PMID:2015900
 A/Accession: S14807
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 668-676 <MA2>
 C/Superfamily: myosin heavy chain; myosin motor domain homology
 C/Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle
 P:21-676/Domain: light meromyosin <LME>

Query Match 24.6%; Score 63.5; DB 2; Length 676;
 Best Local Similarity 35.1%; Pred. No. 24;
 Matches 20; Conservative 13; Mismatches 13; Indels 11; Gaps 3;

Qy 1 GKEETPVQKCORLQIEMNELNEVAALQVDRKVA--DEE---KQSYDAVVAIVTIST 51
 Db 290 GSLHEBEKILRIQLELNQVKS-----IDRKIAKDEMDIQLRNHLRVESMST 341

RESULT 9
 S52696
 myosin heavy chain - rainbow trout (fragment)
 C/Species: Oncorhynchus mykiss (rainbow trout)
 C/Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C/Accession: S52696
 R/Gauvre, L.L.; Fauconneau, B.B.
 submitted to the EMBL Data Library, March 1995
 A/Description: Cloning of a fast skeletal myosin heavy chain expressed both in embryo an
 A/Reference number: S52696
 A/Accession: S52696
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-698 <GAV>
 A/Cross-references: UNIPROT:Q91208; EMBL:Z48794; NID:G755770; PIDN:CAA88724.1; PID:G7557
 A/Superfamily: myosin heavy chain; myosin motor domain homology
 C/Keywords: ATP

Query Match 24.6%; Score 63.5; DB 2; Length 698;
 Best Local Similarity 36.8%; Pred. No. 24;
 Matches 21; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 1 GKEETPVQKCORLQIEMNELNEVAALQVDRKVA--DEE---KQSYDAVVAIVTIST 51
 Db 312 GTLHEBEKILRIQLELNQVKS-----VDRKIAKDEMDIQLRNHLRVESMST 363

RESULT 10
 JX0178
 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken
 N/Contains: myosin ATPase (RC 3.6.4.1)
 C/Species: Gallus gallus (chicken)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: PX0050; PX0051; JX0178; A26365; S02082; PW0009; S39081; S24351; S05
 J/Hayashida, M.; Maeda, T.; Matsuda, G.
 J. Biochem. 110, 54-59, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the
 A/Reference number: PX0050; MUID:92041767; PMID:1939027
 A/Accession: PX0050
 A/Molecule type: protein
 A/Residues: 1-205 <HAY>
 A/Cross-references: UNIPROT:Q90913; UNIPROT:Q90909
 R/Konine, Y.; Maeda, T.; Matsuda, G.
 J. Biochem. 110, 60-67, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of th
 A/Reference number: PX0051; MUID:92041768; PMID:1939028
 A/Accession: PX0051
 A/Molecule type: protein
 A/Residues: 206-636 <KOM>
 R/Maeda, T.; Miyamoto, T.; Matsuzono, K.; Tanaka, Y.; Matsuda, G.

J. Biochem. 110, 68-74, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of t
A:Reference number: EX0052; MUID:92041769; PMID:1935028
A:Accession: EX0052
A:Molecule type: protein
A:Residues: 201-213/632-637 <MA1>
J:Malta, T.; Yajima, E.; Nagata, S.; Miyaniishi, T.; Nakayama, S.; Matsuda, G.
J. Biochem. 110, 75-87, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of th
A:Reference number: UX0178; MUID:92041770; PMID:1935030
A:Accession: UX0178
A:Molecule type: protein
A:Residues: 833-1938 <MA2>
J:Malta, T.; Hayashida, M.; Tanioka, Y.; Komine, Y.; Matsuda, G.
Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987
A:Title: The primary structure of the myosin head.
A:Reference number: A26365; MUID:87092420; PMID:3467365
A:Accession: A26365
A:Molecule type: protein
A:Residues: 1-129, 'X', 131-139, 141-550, 'X', 552-754, 'X', 756-784, 'QL', 787-804, 806-810 <MA3>
J:Matanabe, B.
A:Title: Chem. Hoppe-Seyler 370, 55-61, 1989
A:Title: Amino-acid sequence of the hinge region in chicken myosin subfragment-2.
A:Reference number: S02082; MUID:89228549; PMID:2713098
A:Accession: S02082
A:Molecule type: protein
A:Residues: 1144-1270 <MAT>
J:Yajima, E.
Nagaaki Igakai Zasshi 65, 409-430, 1990
A:Title: Study on tail region of skeletal muscle myosin, primary structure and protease
A:Reference number: PM0009
A:Accession: PM0009
A:Molecule type: protein
A:Residues: 1304-1938 <YAJ>
J:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
submitted to the EMBL Data Library, August 1991
A:Description: Analysis of the chicken fast myosin heavy chain family: Localization of i
A:Reference number: S39081
A:Accession: S39081
A:Molecule type: mRNA
A:Residues: 1081-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1795, 'HV', 1798-1829, 'S', 1831
A:CROSS-references: EMBL:M74084
J:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
A:Reference number: S24348; MUID:92309413; PMID:1377278
A:Accession: S24351
A:Molecule type: mRNA
A:Residues: 1082-1182, 'T', 1184-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1780, 'W', 1782-
A:CROSS-references: EMBL:M74084
J:Matanabe, B.
A:Title: Chem. Hoppe-Seyler 370, 1027-1034, 1989
A:Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal muscle
A:Reference number: S05515; MUID:90121764; PMID:2610940
A:Accession: S05515
A:Molecule type: protein
A:Residues: 842-906, 'Q', 908-1270 <MA3>
J:Matanabe, B.
A:Title: Chem. Hoppe-Seyler 370, 549-558, 1989
A:Title: Amino-acid sequence of the short subfragment-2 in adult chicken skeletal muscle
A:Reference number: S04501; MUID:89374803; PMID:2775482
A:Accession: S04501
A:Molecule type: protein
A:Residues: 852-906, 'Q', 908-1108 <MA2>
J:Matanabe, G.; Malta, T.; Miyaniishi, T.; Hayashida, M.
J. Protein Chem. 6, 33-46, 1987
A:Title: Structure and function of muscle myosin.
A:Reference number: A60877
A:Accession: A60877
A:Molecule type: protein
A:Residues: 1-139, 141-205 <MA1>
J:Gulick, J.; Kropp, K.; Robbins, J.
J. Biol. Chem. 260, 14513-14520, 1985

A:Title: The structure of two fast-white myosin heavy chain promoters. A comparative stu
A:Reference number: A92507; MUID:86033956; PMID:2997212
A:Accession: A24124
A:Molecule type: DNA
A:Residues: 'M', 1-168 <GUL>
A:CROSS-references: GB:M13512; GB:M12083; GB:M13510; NID:9212363; PIDN:AAA4896.1; PID:G
J:Kropp, K.; Gulick, J.; Robbins, J.
J. Biol. Chem. 261, 6613-6618, 1986
A:Title: A canonical sequence organization at the 5'-end of the myosin heavy chain genes
A:Reference number: A92587; MUID:86196091; PMID:3009465
A:Accession: C25217
A:Molecule type: DNA
A:Residues: 'M', 1-56, 'T', 58-76, 'I', 78-168 <KRO>
A:CROSS-references: GB:M13515; GB:M13511; NID:9212373; PIDN:AAA4897.1; PID:9555468
C:Comment: This is a fragment of the globular head.
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methylated
F:1-1938/Product: myosin heavy chain #status experimental <MAT>
F:89-768/Domain: myosin motor domain homology <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)
F:550-587/Region: actin binding #status predicted
F:657-679/Region: actin binding #status predicted
F:841-1938/Domain: coiled coil <COI>
F:841-1289/Region: S2
F:852-1108/Domain: short subfragment 2 <SUB2>
F:1290-1938/Region: light meromyosin
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:35/Modified site: N6-methyllysine (Lys) #status experimental
F:130,551/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F:185/Binding site: ATP (Lys) #status predicted
F:697,707/Active site: Cys #status predicted
F:755/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 24.6%; Score 63.5; DB 1; Length 1938;
Best Local Similarity 36.7%; Pred. No. 71;
Matches 18; Conservative 13; Mismatches 7; Indels 11; Gaps 3;

9 KCRLEFMNELNEVALQVDRKVA--DEE---KQSYDAVATVIST 51
Db 1559 KILRLQELRLNOKSE-----IDRKIAEKDERIDQLKKNHRIKIVSMOST 1602

RESULT 11
F64596
hypothetical protein HP0614 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
J:Accession: F64596
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64596
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-111 <TOM>
A:CROSS-references: UNIPROT:O25335; GB:A8000576; GB:A8000511; NID:92313736; PIDN:AA00768f
C:Superfamily: Helicobacter pylori hypothetical protein jhp0557

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Best Local Similarity 40.6%; Pred. No. 4;
Matches 13; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

11 ORLCIEMNELNEVALQVDRKVADEKOSYD 42
Db 12 QALQAKKKLITELAELEAETIKVSERKSSFN 43

RESULT 12
E84283

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 ; Search time 93.246 Seconds
(without alignments)
291.060 Million cell updates/sec

Title: 09782816-52

Perfect score: 258

Sequence: 1 GSKTPYQKCORLQIEMNEL.....ADEKQSYDANVAIVTISTAR 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243.5	94.4	380	Q9V4Y9	Q9V4Y9 drosophila
2	127.5	49.4	388	Q7PZ25	Q7PZ25 anopheles g
3	82	31.8	402	Q9PTG6	Q9PTG6 gallus gall
4	77	29.8	242	Q6CYK1	Q6CYK1 erwinia car
5	75	29.1	405	Q7T3H1	Q7T3H1 brachydanio
6	74	28.7	401	DCRT2	DCRT2 mouse
7	74	28.7	402	Q6A1H5	Q6A1H5 mus musculu
8	73.5	28.5	403	Q6EJ30	Q6EJ30 xenopus lae
9	72.5	28.1	400	DCRT2	DCRT2 human
10	70.5	27.3	403	Q6IRB3	Q6IRB3 homo sapien
11	70.5	27.3	755	Q9JNMI	Q9JNMI arabidopsis
12	70.5	27.3	879	Q9YHDE	Q9YHDE rana catesb
13	70.5	27.3	1937	MYH8	MYH8 human
14	69.5	26.9	230	Q9ZDT9	Q9ZDT9 homo sapien
15	68	26.4	297	Q9YDX9	Q9YDX9 aeropyrum p
16	67.5	26.2	162	Y157	Y157 AQUAE
17	67.5	26.2	338	Q7XVY2	Q7XVY2 xenopus lae
18	67.5	26.2	1939	Q6DF06	Q6DF06 xenopus tro
19	66	25.6	480	Q6H1N5	Q6H1N5 arabidopsis
20	66	25.6	508	Q7XJ08	Q7XJ08 arabidopsis
21	65.5	25.4	1935	Q6NXX3	Q6NXX3 xenopus tro
22	65	25.2	730	YE45	YE45 SCHPO
23	64.5	25.0	157	Q9PK98	Q9PK98 schizosach
24	64.5	25.0	935	Q81734	Q81734 chlamydia m
25	64	24.8	886	RA50	RA50 STILAC
26	63.5	24.6	657	Q81S59	Q81S59 sulfolobus
27	63.5	24.6	698	Q91208	Q91208 spiroplasma
28	63.5	24.6	708	Q9YH07	Q9YH07 rana catesb
29	63.5	24.6	826	Q9YH07	Q9YH07 rana catesb
30	63.5	24.6	1084	MYSS	MYSS RABIT
31	63.5	24.6	1937	Q81P5	Q81P5 oncorhynch

32	63.5	24.6	1938	MYSS	MYSS CHICK
33	63.5	24.6	1941	MYH2	MYH2 HUMAN
34	63.5	24.6	1941	Q86T56	Q86T56 homo sapien
35	63.5	24.6	2664	Q7RELO	Q7RELO plasmodium
36	63	24.4	111	Q25335	Q25335 helicobacter
37	63	24.4	207	Q983X1	Q983X1 rhizobium l
38	63	24.4	716	Q46317	Q46317 carnobacter
39	63	24.4	716	Q9REY3	Q9REY3 carnobacter
40	62.5	24.2	45	Q71108	Q71108 lactobacill
41	62.5	24.2	222	Q9HQ83	Q9HQ83 halobacteri
42	62.5	24.2	469	Q9ESM6	Q9ESM6 mus musculu
43	62.5	24.2	892	Q63939	Q63939 rattus sp.
44	62.5	24.2	1119	P87344	P87344 theagra ch
45	62.5	24.2	1725	Q7RT66	Q7RT66 plasmodium

ALIGNMENTS

RESULT 1

Q9V4Y9 PRELIMINARY; PRT; 380 AA.

AC Q9V4Y9; ID Q9V4Y9; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update) DB CG8269-PA (LD07994P) DN Name=Dmu; ORFNames=CG8269; OS Drosophila melanogaster (Fruit fly). OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila. OX NCBI_TaxID=7227; RN [1] RP SEQUENCE FROM N. A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P., RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hovind D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jitali B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Laesoe P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D., RA Mekullov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon R., Nusken D.R., Pacile J.M., RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., RA Styrcas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.Y., Wassarman D.A., Weisscock G.M., Weissbach J., RA Williams S.M., Woodger M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., RA Yeh R.F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

```
RL Science 287:2185-2195(2000) .
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Chape M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svitskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002) .
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Ceiniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002) .
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamaoka C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002) .
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN EMBL; AE003835; AAF59034.1; -.
DR EMBL; AY061092; AAL28640.1; -.
DR IncAct; Q9V4Y9; -.
DR FlyBase; FBgn0021825; Dm.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynameitin.
DR Pfam; PF04912; Dynameitin; 1.
SQ SEQUENCE 380 AA; 41998 MW; CF7E1D3BFF5989C5 CRC64;

Query Match 94.4%; Score 243.5; DB 2; Length 380;
Best Local Similarity 98.1%; Pred. No. 1e-18; Mismatches 0; Indels 1; Gaps 1;
Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GEEKTPVOKCORLQIENNELNEVAALQVDRKVADEKQSYDAVATVISTAR 53
DB 94 GEEKTPVOKCORLQIENNELNEVAALQVDRKVADEKQSYDAVATVISTAR 145
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ID 07P225 PRELIMINARY; PRT; 388 AA.
AC 07P225;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP9561 (Fragment).
GN Name=agCG52050; ORFNames=ENSGANG00000015420;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; EAA00075.1; -.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynameitin.
DR Pfam; PF04912; Dynameitin; 1.
DR NON TER 1
FT SEQUENCE 388 AA; 43021 MW; 4F5A549B51D52555 CRC64;

Query Match 49.4%; Score 127.5; DB 2; Length 388;
Best Local Similarity 49.1%; Pred. No. 7.5e-06;
Matches 26; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 GEEKTPVOKCORLQIENNELNEVAALQVDRKVADEKQSYDAVATVISTAR 53
DB 94 GEEKTPVOKCORLQIENNELNEVAALQVDRKVADEKQSYDAVATVISTAR 145
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RESULT 3

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ID 09PTG6 PRELIMINARY; PRT; 402 AA.
AC 09PTG6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Dynameitin.
GN Name=p50;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20056093; PubMed=10588646;
RA Valetti C., Wetzel D.M., Schrader M., Hasbani M.J., Gill S.R.,
RA Kreis T.E., Schroer T.A.;
RT "Role of dynameitin in endocytic traffic: effects of dynameitin
RT overexpression and colocalization with CLIP-170."
RL Mol. Biol. Cell 10:4107-4120(1999) .
RN [2]
RP SEQUENCE FROM N.A.
RX Schroer T.A., Gill S.R., Hasbani J., Grego C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF200744; AAT13996.1; -.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynameitin.
DR Pfam; PF04912; Dynameitin; 1.
SQ SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;
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Query Match 31.8%; Score 82; DB 2; Length 402;
Best Local Similarity 48.7%; Pred. No. 0.86;
Matches 19; Conservative 6; Mismatches 12; Indels 2; Gaps 1;
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Qy 1 GEEKTPVQKCRLOIEMNELLNEVVALQVDRKVADEKQ 37
Db 96 GAKETPOQRYORLQHEVQELIRDEQIQSAVKESAAEE 134

RESULT 4
OCYKI PRELIMINARY; PRT; 242 AA.
AC 06CYKI;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=EC44506;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Actin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagsels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmord G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
RM EMBL; BX350851; CAG77401.1;
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 242 AA; 26438 MW; A67C186B12BE240C CRC64;

Query Match 29.8%; Score 77; DB 2; Length 242;
Best Local Similarity 40.9%; Pred. No. 1.8;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 4 ETPVQKCRLOIEMNELLNEVVALQVDRKVADEKQSDAVAT 47
Db 36 EQPDKCRHLPMMARRINQSLAVDSGLALHRSQVDALVFT 79

RESULT 5
O7T3H1 PRELIMINARY; PRT; 405 AA.
AC 07T3H1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Similar to dynactin 2 (P50).
GN ORNames=zgc:63867; (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Casarini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053120; AAH53120.1;
DR ZFIN; ZDB-GENE-040426-1279; zgc:63867.
DR GO; GO:0005669; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR06996; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
SQ SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;

Query Match 29.1%; Score 75; DB 2; Length 405;
Best Local Similarity 43.6%; Pred. No. 5.2;
Matches 17; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GEEKTPVQKCRLOIEMNELLNEVVALQVDRKVADEKQ 39
Db 96 GAKETPOQRYORLQHEVQELIRDEQIQSAVKESAAEE 134

RESULT 6
DCT2_MOUSE STANDARD; PRT; 401 AA.
ID DCT2_MOUSE
AC 09PK08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
DE (P50 dynactin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein
DE 23-48K) (GMP23-48K).
GN Name=Dctn2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Casarini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Scherch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,
RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

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RC TISSUE=Brain;
RX MEDLINE=97289622; PubMed=9144527; DOI=10.1006/dbrc.1997.6447;
RA Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.;
RT "The presence of the 50-kDa subunit of dynein complex in the nerve
RT growth cone.";
RL Biochem. Biophys. Res. Commun. 233:295-299(1997).
RN [3]
RP INTERACTION WITH BICD2.
RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
RA Hoogenraad C.C., Akhmanova A., Howell S.A., Dottiand B.R.,
RA de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.;
RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-
RT dynein pathway by interacting with these complexes.";
RL EMBO J. 20:4041-4054(2001).
CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in karyopse formation
CC during brain development.
CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated
CC with dynein (By similarity). Interacts with BICD2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC -1- DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic
CC and membrane-associated forms in neonates. Levels of membrane-
CC associated form are greatly reduced in the adult.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: BC004613; AAH04613.1; -
DR MGD: MGI:107733; Dctn2.
DR InterPro: IPR006996; Dynameitin.
DR Pfam: PF04912; Dynameitin.1.
KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0 By similarity.
FT DOMAIN 98 131 Coiled coil (Potential).
FT DOMAIN 214 244 Coiled coil (Potential).
SQ SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940EBC CRC64;

Query Match 28.7%; Score 74; DB 1; Length 401;
Best Local Similarity 35.8%; Pred. No. 6.6;
Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

Qy 1 GKEETPVQKQRLQIEMNELNEVAALQVDRKVADEKQSYDAVAVATVISTAR 53
Db 93 GVKETPQOKYQRLHVEQELTTEVEKIKTVKESATBEKLPVVLAKQLALAK 145

RESULT 7
Q6AYH5 PRELIMINARY; PRT; 402 AA.
AC Q6AYH5;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DB Dynein 2.
GN Name=Dctn2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heitlen E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shervenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Kizymanski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC079042; AAH79042.1; -
DR GO: GO:0005869; C:dynactin complex; IEA.
DR GO: GO:0007017; P:microtubule-based process; IEA.
DR InterPro: IPR006996; Dynameitin.
DR Pfam: PF04912; Dynameitin.1.
SQ SEQUENCE 402 AA; 44148 MW; 55033535A4FB052 CRC64;

Query Match 28.7%; Score 74; DB 2; Length 402;
Best Local Similarity 35.8%; Pred. No. 6.7;
Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

Qy 1 GKEETPVQKQRLQIEMNELNEVAALQVDRKVADEKQSYDAVAVATVISTAR 53
Db 94 GVKETPQOKYQRLHVEQELTTEVEKIKTVKESATBEKLPVVLAKQLALAK 146

RESULT 8
Q66J30 PRELIMINARY; PRT; 403 AA.
AC Q66J30;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MGC82128 protein.
GN Name=MGC82128;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Raley U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Klein S., Gerthard D.S.,
 RL Submitted (Aug-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC081081; AAH81081.1; -
 DR InterPro: IPR006996; Dynactin.
 DR Pfam; PF04912; Dynactin; 1.
 SQ SEQUENCE 403 AA; 44737 MW; 86BE8CE54325EF3 CRC64;
 Query Match 28.5%; Score 73.5; DB 2; Length 403;
 Best Local Similarity 45.1%; Pred. No. 7.6;
 Matches 23; Conservative 5; Mismatches 22; Indels 1; Gaps 1;
 Oy 1 GSEKTPQKCORLQIENNELNEVAALQ-VDRKVADEKSYDAVAVATIS 50
 Db 94 GKMETPOOKYGRLLHVEQLTVEKTKSTWAKSEKLPVPAALAKQVAS 144
 RESULT 9
 DCT2 HUMAN STANDARD; PRT; 400 AA.
 ID OI3561; Q96YN2; Q9BW17;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
 DE (p50 dynactin) (DCTN-50) (Dynactin 2).
 GN Name=DCTN2; Synonyms=DCTN50;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96178072; PubMed=6647893; DOI=10.1083/jcb.132.4.617;
 RA Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.,
 RT "Molecular characterization of the 50-KD subunit of dynactin reveals
 RT organization for the complex in chromosome alignment and spindle
 RT organization during mitosis."
 RL J. Cell Biol. 132:617-633(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta, Skin, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hirsch S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshimiyu S., Cantin P., Prange C.,
 RA Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raley U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 1-384 FROM N.A.
 RA Annals J.P., Yu-Jee L.-Y.,
 RT "Human 50 kD dynactin subunit, p50 dynactin, isolated from HeLa
 RT cells."
 RL Submitted (Nov-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-13.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nb810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.,
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides".
 RL Nat. Biotechnol. 21:566-569(2003).
 CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
 CC and plays a role in prometaphase chromosome alignment and spindle
 CC organization during mitosis. May play a role in synapse formation
 CC during brain development.
 CC -1- SUBUNIT: Subunit of dynactin, a multiprotein complex associated
 CC with dynein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
 CC -----
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 DR EMBL; U50733; AAC50423.1; -
 DR EMBL; BC000718; AAH00718.1; -
 DR EMBL; BC000946; AAH00946.1; -
 DR EMBL; BC014083; AAH14083.1; -
 DR EMBL; AY189155; AAC34395.1; -
 DR Genem; HGNC:2712; DCTN2.
 DR MIM; 607376; -
 DR GO; GO:0005813; C:centrosome; TAS.
 DR GO; GO:0005869; C:dynactin complex; TAS.
 DR GO; GO:0000776; C:kinesinore; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007067; P:mitosis; TAS.
 DR InterPro: IPR006996; Dynactin.
 DR Pfam; PF04912; Dynactin; 1.
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
 KW Membrane; Microtubule; Motor protein.
 FT INIT MET 0
 FT DOMAIN 98 131 Coiled coil (potential).
 FT DOMAIN 213 243 Coiled coil (potential).
 FT DOMAIN 378 398 Coiled coil (potential).
 FT CONFLICT 34 34 A -> APAQEL (in Ref. 1).
 FT CONFLICT 35 35 E -> ELE (in Ref. 3).
 FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).
 SQ SEQUENCE 400 AA; 44099 MW; 0A95AE95C0B270F CRC64;
 Query Match 28.1%; Score 72.5; DB 1; Length 400;
 Best Local Similarity 48.7%; Pred. No. 9.7;
 Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 Oy 1 GSEKTPQKCORLQIENNELNEVAALQVD-RKVADEK 38
 Db 93 GKMETPOOKYGRLLHVEQLTVEKTKSTWAKSEKLPVPAALAKQVAS 131
 RESULT 10
 ID O6IRB3 PRELIMINARY; PRT; 403 AA.
 AC O6IRB3;

```
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Dctn2-prov protein.
GN Name=dctn2-prov.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.U., McKernan K.J., Malek J.A., Gunatane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalke D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RT Dev. Dyn. 225:384-391 (2002).
RN
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
RX EMBL; BC070987; AAH70987.1;
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR006996; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
SQ SEQUENCE 403 AA; 44828 MW; 9FD158C7C7983062 CRC64;

Query Match 27.3%; Score 70.5; DB 2; Length 403;
Best Local Similarity 51.3%; Pred. No. 16;
Matches 20; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 GKKETPVQKQRLQIEMNELINEVAALQVD-RKYADEEK 38
Db 94 GIKETPOOKYQRLHVEVQLTQVEVKTKSTLKSATK 132

RESULT 11
Q9LNM1 PRELIMINARY; PRT; 755 AA.
AC Q9LNM1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE F12K21.7.
OS Arabidopsis thaliana (Mouse-ear cress).
```

```
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altairi H., Bei B., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbeky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Eckert J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altairi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharbeky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Eckert J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC023279; AAF79274.1;
DR InterPro; IPR001005; MYB DNA binding.
DR PROSITE; PS00037; MYB 1; UNKNOWN 1.
SQ SEQUENCE 755 AA; 83720 MW; B4DBCB410208022A CRC64;

Query Match 27.3%; Score 70.5; DB 2; Length 755;
Best Local Similarity 36.5%; Pred. No. 31;
Matches 20; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

QY 2 EKETPVQKQRLQIEMNELINEVAALQVD-RKYADEEKQSYAVATYSTAR 53
Db 582 EASRIQAAER---EKNEALSEAAAKLER---EEGRGURSEVAAAIQTTR 626

RESULT 12
Q9YHD8 PRELIMINARY; PRT; 879 AA.
AC Q9YHD8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Myosin heavy chain (Fragment).
GN Name=MHC-1;
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8400;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tall muscle;
RX MEDLINE=99179235; PubMed=10079518;
RX DOI=10.1002/(SICI)1520-6408(1999)24:1/2<151::AID-DVGA4>3.3.CO;2-W;
RA Hu H., Merrifield P., Atkinson B.G.;
RT "Expression of the myosin heavy chain genes in the tail muscle of
RT thyroid hormone-induced metamorphosing Rana catesbeiana tadpoles."
RL Dev. Genet. 24:151-164 (1999).
DR EMBL; AF097904; AAD13769.1;
DR HSSP; P25054; IDEB.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin tail 1; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON TER 1
SQ SEQUENCE 879 AA; 101710 MW; 1C456851E968A3D8 CRC64;

Query Match 27.3%; Score 70.5; DB 2; Length 879;
Best Local Similarity 36.8%; Pred. No. 36;
```


Matches 21; Conservative 11; Mismatches 14; Indels 11; Gaps 3;

Qy 1 GSEKTPVQKCRPQLENNELNEVALLOVDRKVA--DEE---KQSYAVAVATVIST 51
Db 489 GSLHEESKIRIOLELNQKSE-----VDRKIAEKDEEIRIQLKNSQRIDTQST 540

RESULT 13

MYH8 HUMAN STANDARD; PRT; 1937 AA.

AC P13535; Q14910;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Myosin heavy chain, skeletal muscle, perinatal (MYHC-perinatal).
GN Name=MYH8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90323631; PubMed=2373371; DOI=10.1016/0378-1119(90)90020-R;
RA Karsch-Mizrachi I., Peghali R., Shows T.B. Jr., Leitman L.A.;
RT "Generation of a full-length human perinatal myosin heavy-chain-
encoding cDNA.";
RL Gene 89:289-294(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95324556; PubMed=7601129;
RA Ullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,
R Steadman H.H., Rubinstein N.A.;
RT "Characterization of a human perinatal myosin heavy-chain
transcript.";
RL Eur. J. Biochem. 230:1001-1006(1995).
RN [3]
RP SEQUENCE OF 502-1937 FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90235862; PubMed=1691980;
RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goede H.W.,
R Arnold H.H.;
RT "Identification of three developmentally controlled isoforms of human
myosin heavy chains.";
RL Eur. J. Biochem. 189:55-65(1990).
RN [4]
RP SEQUENCE OF 860-1937 FROM N.A.
RX MEDLINE=89234168; PubMed=2715179; DOI=10.1083/jcb.108.5.1791;
RA Peghali R., Leitman L.A.;
RT "Molecular genetic characterization of a developmentally regulated
human perinatal myosin heavy chain.";
RL J. Cell Biol. 108:1791-1797(1989).
RN [5]
RP SEQUENCE OF 1-46 FROM N.A.
RA Esser K., Tichat A., Myszkowski M.;
RT "Isolation and characterization of the human perinatal MHC promoter.";
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
RN [6]
RP VARIANT CARNEY COMPLEX VARIANT/TRISOMY-PSEUDOCAMPDODACTYL SYNDROME
GN GUN-674.
RX PubMed=15282353; DOI=10.1056/NEJMoa040584;
RA Veugelers M., Bressan M., McDermott D.A., Wermowicz S., Morton C.C.,
R Mabry C.C., Lefevre J.-F., Zunanon A., Destree A., Chaudron J.-M.,
RA Baeson C.T.;
RT "Mutation of perinatal myosin heavy chain associated with a Carney
complex variant.";
RL N. Engl. J. Med. 351:460-469(2004).
CC -1- FUNCTION: Muscle contraction.
CC -1- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2
heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
and 2 regulatory light chain subunits (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing
cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
characteristic for alpha-helical coiled coils.
CC -1- DISEASE: Defects in MYH8 are a cause of Carney complex variant
[MIM:60837]. Carney complex is a multiple neoplasia syndrome
characterized by spotty skin pigmentation, cardiac and other
myxomas, endocrine tumors, and psammomatous melanotic schwannomas.
Familial cardiac myxomas are associated with spotty pigmentation
of the skin and other phenotypes, including primary pigmented
nodular adrenocortical dysplasia, extracardiac (frequently
cutaneous) myxomas, schwannomas, and pituitary, thyroid,
testicular, bone, ovarian, and breast tumors. Cardiac myxomas do
not develop in all patients with the Carney complex, but affected
patients have at least two features of the complex or one feature
and a clinically significant family history.
CC -1- DISEASE: Defects in MYH8 are a cause of trisomy-
pseudocampodactyly syndrome [MIM:18300]; also called Hecht-Beals
or Dutch-Kentucky syndrome. The trisomy-pseudocampodactyly
syndrome is a hereditary distal arthroproposis characterized by an
inability to open the mouth fully (trisismus) and
pseudocampodactyly in which wrist dorsiflexion, but not
volarflexion, produces involuntary flexion contracture of distal
and proximal interphalangeal joints. Such hand and jaw
contractures are caused by shortened flexor muscle-tendon units.
Similar lower-limb contractures also produce foot deformity. The
trisismus-pseudocampodactyly syndrome is a morbid autosomal
dominant trait with variable expressivity but high penetrance. In
these patients, trismus complicates dental care, feeding during
infancy, and intubation for anesthesia, and the
pseudocampodactyly impairs manual dexterity, with consequent
occupational and social disability. Many patients require surgical
correction of contractures.
CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
meromyosin (LMW) and 1 heavy meromyosin (HWM). It can later be
split further into 2 globular subfragments (S1) and 1 rod-shaped
subfragment (S2).
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M36769; AAC17185.1; -;
DR EMBL; Z38133; CA86293.1; -;
DR EMBL; X51592; CAA35941.1; -;
DR EMBL; AF067143; AAC21557.1; -;
DR PIR; I38055; I38055.
DR HSSP; P13538; 2MYS.
DR GeneW; HGNC:7578; MYH8.
DR MIM; 160741; -;
DR MIM; 60837; -;
DR MIM; 158300; -;
DR GO; GO:0005859; C:muscle myosin; TAS.
DR GO; GO:0008307; F:structural constituent of muscle; TAS.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; Myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRODOM; PD000355; MYOSINHEAD; 1.
DR PROSITE; PS50096; IQ; 1.
DR Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;
KW Disease mutation; Methylation; Multigene family; Muscle protein;
KW Myosin; Thick filament.

FT DOMAIN 1 780 Myosin head-like.
FT DOMAIN 781 813 IO.
FT DOMAIN 842 1937 Coiled coil (potential).
FT NP_BIND 181 188 ATP.
FT DOMAIN 658 680 Actin-binding.
FT DOMAIN 760 774 Actin-binding.
FT MOD_RES 132 132 N6,N6,N6-trimethyllysine (potential).
FT VARIANT 674 674 R -> Q (in Carney complex variant and trismus-pseudocamptodactyly syndrome).
/FTid=VAR_019810
FT CONFLICT 15 15 A -> R (in Ref. 2).
FT CONFLICT 970 970 E -> Q (in Ref. 1 and 4).
FT CONFLICT 1072 1072 M -> N (in Ref. 3).
FT CONFLICT 1247 1247 N -> H (in Ref. 1 and 4).
FT CONFLICT 1251 1252 MC -> DGG (in Ref. 3).
FT CONFLICT 1261 1261 E -> G (in Ref. 1 and 4).
FT CONFLICT 1297 1297 K -> Q (in Ref. 1 and 4).
FT CONFLICT 1377 1378 KY -> NT (in Ref. 3).
FT CONFLICT 1504 1505 EN -> AH (in Ref. 1 and 4).
FT CONFLICT 1847 1847 E -> D (in Ref. 1 and 4).
FT CONFLICT 1914 1914 D -> H (in Ref. 2).
SQ SEQUENCE 1937 AA; 222762 MW; A3ER2D151792B9B8 CRC64;

Query Match 27.3%; Score 70.5; DB 1; Length 1937;
Best Local Similarity 28.9%; Pred. No. 80;
Matches 22; Conservative 15; Mismatches 8; Indels 31; Gaps 4;

Qy 2 EKERPVOKQ-----RLQIEMNELLNEVALQVDRKVA--DEE-- 37
Db 1533 KKQVEQCECEIQALIEAEASLEHEGKILRIQLELNQKSE---VDRKIAEKDEID 1587
Qy 38 --KQSYDAVAVTIST 51
Db 1588 QLKXNHRVETMOST 1603

RESULT 14
ID Q92DT9 PRELIMINARY; PRT; 230 AA.
AC Q92DT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin0723 protein.
GN OrderedLocustNames=lin0723;
OS Listeria innocua
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
BAguero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domain E., Dominguez-Bernal G., Duchaud E., Durrant L., Dussauget O.,
RA Entian K.-D., Feshi H., Garcia-del Portillo F., Garrido P.,
GAutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kun M., Kuntz F., Kurapkat G.,
RAMadueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RT "Comparative genomics of Listeria species".
RL Science 294:849-852(2001).
DR EMBL; AL596166; CAC95955.1; -.
DR PIR; AC1523; AC1523.
DR ListList; LIN0723; -.
KW Complete proteome.
SQ SEQUENCE 230 AA; 27050 MW; 05ACFPB3B8B71D CRC64;

Query Match 26.9%; Score 69.5; DB 2; Length 230;
Best Local Similarity 30.5%; Pred. No. 12;

Matches 18; Conservative 10; Mismatches 16; Indels 15; Gaps 1;
Qy 2 EKERPVOK-----CQRLQIEMNELLNEVALQVDRKVADEEKOSYDAVV 45
Db 33 EVESPYKEBLENNHOKELKMSAIEIEQOKLANEKAAIKERQAIIEELKQSAEAI 91

RESULT 15
ID Q9YDX9 PRELIMINARY; PRT; 297 AA.
AC Q9YDX9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ABE0790.
GN OrderedLocustNames=ABE0790;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;
OX Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankael A., Kosugi H.,
RA Hosooyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix KI.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000060; BAA79768.1; -.
DR PIR; H72670; H72670.
DR HSSP; O15813; ID7M.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 297 AA; 35816 MW; CBBFF3961063E5B8 CRC64;

Query Match 26.4%; Score 68; DB 2; Length 297;
Best Local Similarity 46.7%; Pred. No. 23;
Matches 14; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 12 RLQIEMNELLNEVALQVDRKVADEKQSY 41
Db 29 RLKERERKLINNEVALREBRKASREKREY 58
Search completed: November 3, 2005, 22:03:06
Job time : 95.246 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:51:39 ; Search time 27.2086 Seconds
(without alignments)
145.410 Million cell updates/sec

Title: 09782816-52

Perfect score: 258

Sequence: 1 GKEKTPVQKCORLQIENNEL.....ADEKQSYDAVAVTISTAR 53

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	62.0	142	4	US-09-270-767-43370
2	70.5	27.3	1937	4	US-09-538-092-918
3	62.5	24.2	1939	4	US-09-538-092-915
4	62.5	24.2	1939	4	US-09-949-016-11104
5	61.5	23.8	1939	4	US-09-949-016-6925
6	61.5	23.8	1942	4	US-09-949-016-8135
7	59.5	23.1	1940	4	US-09-538-092-901
8	59.5	23.1	1963	4	US-09-949-016-8888
9	58	22.5	1248	2	US-09-080-897-2
10	58	22.5	1248	2	US-09-323-735-2
11	58	22.5	1255	3	US-09-080-897-4
12	58	22.5	1255	3	US-08-899-595-1
13	58	22.5	1255	3	US-09-323-735-4
14	58	22.5	1315	3	US-08-899-595-3
15	58	22.5	1413	3	US-09-252-991A-23627
16	57	22.1	203	4	US-09-711-164-436
17	57	22.1	203	5	PCT-US94-01149-14
18	57	22.1	304	5	PCT-US94-01149-55
19	57	22.1	304	5	PCT-US94-01149-57
20	57	22.1	585	2	US-08-453-848-11
21	57	22.1	585	3	US-09-169-027-11
22	57	22.1	586	2	US-08-453-848-19
23	57	22.1	586	2	US-09-169-027-19
24	57	22.1	589	2	US-08-453-848-13
25	57	22.1	589	2	US-09-169-027-13
26	57	22.1	592	2	US-08-453-848-17
27	57	22.1	592	3	US-09-169-027-17

28	57	22.1	1686	4	US-09-355-160D-2	Sequence 2, Appli
29	57	22.1	1686	4	US-10-092-219-2	Sequence 2, Appli
30	56.5	21.9	231	4	US-09-270-767-58576	Sequence 58576, A
31	56.5	21.9	442	4	US-09-270-767-43234	Sequence 43234, A
32	56	21.7	179	4	US-09-270-767-60196	Sequence 60196, A
33	56	21.7	592	4	US-09-919-039-141	Sequence 141, App
34	56	21.7	632	4	US-09-949-016-10668	Sequence 10668, A
35	56	21.7	961	4	US-09-914-259-66	Sequence 66, Appl
36	56	21.7	1572	4	US-09-562-702A-32	Sequence 32, Appl
37	56	21.7	1572	4	US-09-561-818A-28	Sequence 28, Appl
38	56	21.7	1605	4	US-09-562-702A-30	Sequence 30, Appl
39	56	21.7	1605	4	US-09-561-818A-26	Sequence 26, Appl
40	55.5	21.5	319	3	US-08-872-979-1	Sequence 1, Appli
41	55.5	21.5	953	4	US-09-252-991A-21559	Sequence 21559, A
42	55.5	21.5	1938	4	US-09-949-016-6417	Sequence 6417, Ap
43	55.5	21.5	1959	4	US-09-949-016-8134	Sequence 8134, Ap
44	55	21.3	182	4	US-09-248-796A-14143	Sequence 14143, A
45	55	21.3	208	4	US-09-248-796A-19287	Sequence 19287, A

ALIGNMENTS

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RESULT 1
US-09-270-767-43370
; Sequence 43370, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 43370
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43370

Query Match          62.0%; Score 160; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GKEKTPVQKCORLQIENNELNEVALQVDRK 32
Db 111 GKEKTPVQKCORLQIENNELNEVALQVDRK 142

RESULT 2
US-09-538-092-918
; Sequence 918, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gluc, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 918
; LENGTH: 1937
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918

Query Match      27.3%; Score 70.5; DB 4; Length 1937;
Best Local Similarity 28.9%; Pred. No. 1.1;
Matches 22; Conservative 15; Mismatches 8; Indels 31; Gaps 4;

QY      2 EKRPVQCCO-----PLQIEMNMLNEVALQVDRKVA--DEE-- 37
DB      1533 KQVQECCETQALMEBAASLHEEGKILRIQLNELNVKSE-----VDKRIAEKDESID 1587
QY      38 --KQSYDAVAVATVIST 51
DB      1588 QLRKNHTRVETMST 1603

RESULT 3
US-09-538-092-915
; Sequence 915, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gloc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 915
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P12882
US-09-538-092-915

Query Match      24.2%; Score 62.5; DB 4; Length 1939;
Best Local Similarity 32.7%; Pred. No. 15;
Matches 16; Conservative 14; Mismatches 8; Indels 11; Gaps 2;

QY      9 KCORLQIEMNMLNEVALQVDRKVA-----DEEKQSYDAVAVATVIST 51
DB      1561 KILRIQLNELNVKSE-----VDKRIAEKDESIDQKRNHTRVETMST 1604

RESULT 4
US-09-949-016-11104
; Sequence 1104, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11104

; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11104

Query Match      24.2%; Score 62.5; DB 4; Length 1939;
Best Local Similarity 32.7%; Pred. No. 15;
Matches 16; Conservative 14; Mismatches 8; Indels 11; Gaps 2;

QY      9 KCORLQIEMNMLNEVALQVDRKVA-----DEEKQSYDAVAVATVIST 51
DB      1561 KILRIQLNELNVKSE-----VDKRIAEKDESIDQKRNHTRVETMST 1604

RESULT 5
US-09-949-016-6925
; Sequence 6925, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6925
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6925

Query Match      23.8%; Score 61.5; DB 4; Length 1939;
Best Local Similarity 36.7%; Pred. No. 21;
Matches 18; Conservative 13; Mismatches 7; Indels 11; Gaps 3;

QY      9 KCORLQIEMNMLNEVALQVDRKVA-----DEEKQSYDAVAVATVIST 51
DB      1561 KILRIQLNELNVKSE-----IDKRIAEKDESIDQKRNHTRVETMST 1604

RESULT 6
US-09-949-016-8135
; Sequence 8135, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8135
; LENGTH: 1942
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8135
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Query Match	23.1%;	Score 59.5;	DB 4;	Length 1963;
Best Local Similarity	35.4%;	Pred. No. 41;		
Matches 17;	Conservative 11;	Mismatches 9;	Indels 11;	Gaps 3;

RESULT 10
 US-09-323-735-2
 ? Sequence 2, Application US/09323735
 ? Patent No. 6197932
 ? GENERAL INFORMATION:
 ? APPLICANT: King, Mary-Claire
 ? APPLICANT: Lynch, Eric D.
 ? APPLICANT: Lee, Ming
 ? APPLICANT: Morrow, Jan E.
 ? APPLICANT: Welsh, Birt L.
 ? APPLICANT: Leon, Pedro E.
 ? TITLE OF INVENTION: Modulators of Actin
 ? NUMBER OF SEQUENCES: 14
 ? CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-323-735-2

Query Match 22.5%; Score 58; DB 3; Length 1248;
Best Local Similarity 34.0%; Pred. No. 37;
Matches 16; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

Oy 2 EKETPVOKCRLQIEMNELINVEALQVDRKVADEKQSYDAVVA--TVISTA 48
Db 517 EKQIATKQKDLBAVSKLTGEVAKLTSELEDAKNEMASISAVVAVSVSSSA 563

RESULT 11
US-09-080-897-4
Sequence 4, Application US/09080897
Patent No. 5985574
GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welch, Pili L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-080-897-4

Query Match 22.5%; Score 58; DB 2; Length 1255;
Best Local Similarity 35.8%; Pred. No. 37;
Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

Oy 2 EKETPVOKCRLQIEMNELINVEALQVDRKVADEKQSYDAVVA--TVISTA 52
Db 517 EKQIATKQKDLBAVSKLTGEVAKLTSELEDAKNEMASISAVVAVSVSSSA 569

RESULT 12
US-08-899-595-1
Sequence 1, Application US/08899595
Patent No. 611072
GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 611072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 049441/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-595-1

Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

QY 2 EKETPVQKQRLQIEMNELNEVALQVDRVADBEKQSYDAVVA--TVISTA 52
Db 517 EKQOITAKODLEAVSKLTGEVAKLTKELEDAKKEMASLSAVVAVPSVSSA 569

RESULT 13

US-09-323-735-4
Sequence 4, Application US/09323735
Patent No. 6197932
GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welch, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-323-735-4

Query Match 22.5%; Score 58; DB 3; Length 1355;
Best Local Similarity 35.8%; Pred. No. 37;
Matches 19; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

QY 2 EKETPVQKQRLQIEMNELNEVALQVDRVADBEKQSYDAVVA--TVISTA 52
Db 517 EKQOITAKODLEAVSKLTGEVAKLTKELEDAKKEMASLSAVVAVPSVSSA 569

RESULT 14

US-08-899-595-3
Sequence 3, Application US/08899595
Patent No. 611072
GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 611072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 049441/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-595-3

Query Match 22.5%; Score 58; DB 3; Length 1315;
Best Local Similarity 34.0%; Pred. No. 39;
Matches 16; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 2 EKETPVQKQRLQIEMNELNEVALQVDRVADBEKQSYDAVVA 48
Db 569 EKQOITAKODLEAVSKLTGEVAKLTKELEDAKKEMASLSAAITV 615

RESULT 15

US-09-252-991A-23627
Sequence 23627, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23627
LENGTH: 1413
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23627

Query Match 22.5%; Score 58; DB 4; Length 1413;
Best Local Similarity 31.5%; Pred. No. 43;
Matches 17; Conservative 11; Mismatches 16; Indels 10; Gaps 2;

Mon Nov 7 09:42:39 2005

09782816-52.ra1

Page 6

QY 6 PVQCKQR---LQIEMNELLNEVALQVDRKYAD-----EEKQSYDAVATVI 49
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Job time : 28.2086 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:53:15 ; Search time 95.5134 Seconds
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232.174 Million cell updates/sec

Title: 09782816-52

Perfect score: 258
Sequence: 1 GKEKTPVQKCRLOIEMNEL.....ADEKQSYDAVAVATISTAR 53

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Published Applications AA:*

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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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- 23: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	114	44.2	22	10	US-09-782-816A-26
5	108	41.9	21	10	US-09-782-816A-27
6	105	40.7	22	10	US-09-782-816A-2
7	103	39.9	20	10	US-09-782-816A-28
8	98	38.0	19	10	US-09-782-816A-29
9	93	36.0	18	10	US-09-782-816A-30
10	88	34.1	17	10	US-09-782-816A-31
11	81	31.4	16	10	US-09-782-816A-32

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	74	28.7	224	16	US-10-425-115-315831	Sequence 315831,																													
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	72.5	28.1	406	10	US-09-782-816A-53	Sequence 53, Appl																													
	72.5	28.1	465	9	US-09-925-298-676	Sequence 676, App																													
	72.5	28.1	465	14	US-10-102-806-676	Sequence 676, App																													
	72	27.9	14	10	US-09-782-816A-34	Sequence 34, Appl																													
	70.5	27.3	1937	16	US-10-723-860-106	Sequence 106, App																													
	70.5	27.3	1937	16	US-10-723-860-106	Sequence 106, App																													
	69.5	26.9	13	9	US-09-864-761-43401	Sequence 43401, A																													
	67	26.0	886	17	US-10-732-923-3311	Sequence 3311, Appl																													
	64	24.8	185	15	US-10-424-599-207072	Sequence 3311, Ap																													
	63.5	24.6	185	15	US-10-424-599-207072	Sequence 207072,																													
	63.5	24.6	233	15	US-10-425-114-48404	Sequence 48404, A																													
	63.5	24.6	324	15	US-10-424-599-207069	Sequence 207069,																													
	62.5	24.2	97	9	US-09-864-761-39043	Sequence 39043, A																													
	62.5	24.2	103	9	US-09-864-761-42193	Sequence 42193, A																													
	62.5	24.2	141	17	US-10-805-684-134	Sequence 134, App																													
	62.5	24.2	1939	16	US-10-205-219-102	Sequence 102, App																													
	62.5	24.2	1939	17	US-10-408-765A-2188	Sequence 2188, Ap																													
	62.5	24.2	1939	17	US-10-805-684-152	Sequence 152, App																													
	62	24.0	351	16	US-10-821-273-26	Sequence 26, Appl																													
	61.5	23.8	97	9	US-09-864-761-42176	Sequence 42176, A																													
	61.5	23.8	483	15	US-10-424-599-170198	Sequence 170198,																													
	61.5	23.8	1948	18	US-10-450-763-51592	Sequence 51592, A																													
	61.5	23.6	1985	17	US-10-732-923-3351	Sequence 3351, Ap																													
	60	23.3	245	16	US-10-767-701-41002	Sequence 41002, A																													
	60	23.3	1042	16	US-10-408-765A-1655	Sequence 1655, Ap																													
	59.5	23.1	1167	16	US-10-723-860-54	Sequence 54, Appl																													
	59.5	23.1	1940	10	US-09-738-630-99	Sequence 99, Appl																													
	59.5	23.1	1940	16	US-10-408-765A-1175	Sequence 1175, Ap																													
	59	22.9	110	15	US-10-335-977-8524	Sequence 8524, Ap																													

ALIGNMENTS

RESULT 1
US-09-782-816A-52
Sequence 52, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069,001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 53
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-52

Query Match 100.0%; Score 258; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKEKTPVQKCRLOIEMNELNEVAALQVDKRVADDEKQSYDAVAVATISTAR 53
DB 1 GKEKTPVQKCRLOIEMNELNEVAALQVDKRVADDEKQSYDAVAVATISTAR 53

RESULT 2
US-09-782-816A-56
Sequence 56, Application US/09782816A
Publication No. US20030032771A1

```
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT FILING DATE: US/09/782,816A
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-56
```

```
Query Match          94.4%; Score 243.5; DB 10; Length 380;
Best Local Similarity 98.1%; Pred. No. 1.6e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Oy      1 GKEKTPVQKQRLQIEMNELINEVAALQVDRKVADEEKOSYDAVATVISTAR 53
Db      94 GKEKTPVQKQRLQIEMNELINEVAALQVDRKVADEEKOSYDA-VATVISTAR 145
```

```
RESULT 3
US-11-097-143-4056
; Sequence 4056, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT FILING DATE: 2005-04-04
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4056
; LENGTH: 380
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4056
```

```
Query Match          94.4%; Score 243.5; DB 20; Length 380;
Best Local Similarity 98.1%; Pred. No. 1.6e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Oy      1 GKEKTPVQKQRLQIEMNELINEVAALQVDRKVADEEKOSYDAVATVISTAR 53
Db      94 GKEKTPVQKQRLQIEMNELINEVAALQVDRKVADEEKOSYDA-VATVISTAR 145
```

RESULT 4

```
US-09-782-816A-26
; Sequence 26, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT FILING DATE: US/09/782,816A
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-26
```

```
Query Match          44.2%; Score 114; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 GKEKTPVQKQRLQIEMNELIN 22
Db      1 GKEKTPVQKQRLQIEMNELIN 22
```

```
RESULT 5
US-09-782-816A-27
; Sequence 27, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT FILING DATE: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-27
```

```
Query Match          41.9%; Score 108; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2 EKETPVQKQRLQIEMNELIN 22
Db      1 EKETPVQKQRLQIEMNELIN 21
```

```
RESULT 6
US-09-782-816A-2
; Sequence 2, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT FILING DATE: US/09/782,816A
; NUMBER OF SEQ ID NOS: 56
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-2

Query Match      40.7%; Score 105; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 EVAALQVDRKVADEKOSYDAV 44
Db      1 EVAALQVDRKVADEKOSYDAV 22

RESULT 7
US-09-782-816A-28
; Sequence 28, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-28

Query Match      39.9%; Score 103; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KETPVQKCRLOIEMNELN 22
Db      1 KETPVQKCRLOIEMNELN 20

RESULT 8
US-09-782-816A-29
; Sequence 29, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-29

Query Match      38.0%; Score 98; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ETPVQKCRLOIEMNELN 22
Db      1 ETPVQKCRLOIEMNELN 22
```

```
Db      1 ETPVQKCRLOIEMNELN 19

RESULT 9
US-09-782-816A-30
; Sequence 30, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-30

Query Match      36.0%; Score 93; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TPVQKCRLOIEMNELN 22
Db      1 TPVQKCRLOIEMNELN 18

RESULT 10
US-09-782-816A-31
; Sequence 31, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-31

Query Match      34.1%; Score 88; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PVQKCRLOIEMNELN 22
Db      1 PVQKCRLOIEMNELN 17

RESULT 11
US-09-782-816A-32
; Sequence 32, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
```

FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 16
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-32

Query Match 31.4%; Score 81; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VQKQRLQIEMNELN 22
DB 1 VQKQRLQIEMNELN 16

RESULT 12
US-09-782-816A-33

Sequence 33, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 15
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-782-816A-33

Query Match 29.8%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 OKCQRLQIEMNELN 22
DB 1 OKCQRLQIEMNELN 15

RESULT 13
US-09-782-816A-54

Sequence 54, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 183
TYPE: PRT
ORGANISM: Mus musculus
US-09-782-816A-54

Query Match 28.7%; Score 74; DB 10; Length 183;
Best Local Similarity 35.8%; Pred. No. 0.32;

Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 GKEKTPVQKQRLQIEMNELNEVAALQVDRKVADEKOSYDAVATVISTAR 53
DB 94 GVKETPOOKYORLHVEQELTTEVEKIKITVKSATESKLPVVALQALAK 146

RESULT 14
US-10-425-115-315831
Sequence 315831, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 315831
LENGTH: 224
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_51109C.1.dep
US-10-425-115-315831

Query Match 28.7%; Score 74; DB 16; Length 224;
Best Local Similarity 35.8%; Pred. No. 0.41;
Matches 19; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 GKEKTPVQKQRLQIEMNELNEVAALQVDRKVADEKOSYDAVATVISTAR 53
DB 47 GVKETPOOKYORLHVEQELTTEVEKIKITVKSATESKLPVVALQALAK 99

RESULT 15
US-09-782-816A-51

Sequence 51, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 52
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: UNSURE
LOCATION: 44
OTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-51

Query Match 28.1%; Score 72.5; DB 10; Length 52;
Best Local Similarity 48.7%; Pred. No. 0.1;
Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 GKEKTPVQKQRLQIEMNELNEVAALQVD-RKYADEBK 38
DB 1 GVKETPOOKYORLHVEQELTTEVEKIKITVKSATESK 39

Mon Nov 7 09:42:39 2005

09782816-52.rapb

Page 5

Search completed: November 3, 2005, 22:11:41
Job time : 96.5134 secs

959

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 18.9091 Seconds
(without alignments)
264.596 Million cell updates/sec

Title: 09782816-51

Sequence: 1 GVKETPOQKQRLHVEVQEL.....ESATREKLTPLAKQLAAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.5	27.7	804	2	TJ2864
2	68	27.1	1742	2	T49451
3	67.5	26.9	1325	2	T49451
4	67	26.7	1281	2	TJ2235
5	67	26.7	2481	2	D80011
6	66	26.3	393	2	T04957
7	66	26.3	866	2	C71509
8	65.5	26.1	1837	2	T41023
9	64	25.5	210	2	B84499
10	63.5	25.3	163	2	S69518
11	63.5	25.3	374	2	D70391
12	63	25.1	281	2	F75216
13	63	25.1	314	2	F90577
14	62.5	24.9	1281	2	JCS368
15	62	24.7	296	2	TJ2222
16	62	24.7	2469	2	H36812
17	61	24.3	442	2	C95070
18	61	24.3	442	2	A97938
19	60.5	24.1	819	2	AC2029
20	60.5	24.1	1214	2	JC2069
21	60	23.9	523	2	S06920
22	60	23.9	695	2	H72243
23	59.5	23.7	279	2	D71453
24	59.5	23.7	665	2	S62328
25	59	23.5	112	2	G72645
26	59	23.5	239	2	D84004
27	59	23.5	550	2	G85436
28	59	23.5	611	2	E90543
29	59	23.5	782	2	A34219

30	59	23.5	951	2	T45726	hypothetical prote
31	59	23.5	2101	2	A42184	nuclear mitotic ap
32	58.5	23.3	154	2	T25602	hypothetical prote
33	58.5	23.3	821	2	A12417	hypothetical prote
34	58	23.1	302	2	T01615	hypothetical prote
35	58	23.1	319	2	T25666	hypothetical prote
36	58	23.1	623	2	A48315	hypothetical prote
37	58	23.1	630	2	D97992	lamin III - Africa
38	58	23.1	677	2	T22333	hypothetical prote
39	58	23.1	707	2	S78538	histidine ammonia-
40	58	23.1	727	2	AD2188	site-specific reco
41	58	23.1	740	2	G95153	hypothetical prote
42	58	23.1	978	2	A70387	neuraminidase, pro
43	58	23.1	2139	2	T18296	conserved hypother
44	58	23.1	2422	2	T12687	myosin heavy chain
45	57.5	22.9	237	2	C87656	AKR protein homolo
						GGDEF family prote

ALIGNMENTS

```

RESULT 1
TJ2864
hypothetical protein ZK484.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: TJ2864
R/Murray, J.; Mohlmann, P.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid ZK484.
A/Reference number: Z21237
A/Accession: TJ2864
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-804 <MIR>
A/Cross-references: UNIPROT:Q95X56; EMBL:AF040659; PDB:1AAB95062.1; GSPDB:GN00019; CESP:
A/Experimental source: strain Bristol N2; clone ZK484
C/Genetics:
A/Gene: CESP:ZK484.4
A/Map position: 1
A/Introns: 52/1; 113/1; 162/3; 201/3; 248/2; 346/1; 433/2; 464/3; 565/3; 628/2; 646/3; 7
C/Superfamily: Caenorhabditis elegans hypothetical protein ZK484.4

Query Match 27.7%; Score 69.5; DB 2; Length 804;
Best local similarity 34.4%; Pred. No. 20;
Matches 22; Conservative 10; Mismatches 19; Indels 13; Gaps 3;

QY 2 VKETPOQKQRLHVEVQELTTEV-----KTKT-TVKSATRE-KLTPVLAKQ 48
DB 366 VEDTPDEKYQKTKTVSEIENNEEDGIGASTSKRTVTIKEDIEVVKQTPVAKLRA 425

OY 49 LAAL 52
DB 426 SAKL 429

RESULT 2
T49451
kinasin-like protein Kif2a related protein [imported] - Neurospora crassa
N/Alternate names: protein B14D6.30
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
R/Schulte, U.; Aign, V.; Hohnsbeil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022
A/Accession: T49451
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1742 <SCH>
A/Cross-references: UNIPROT:Q8X0C5; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.30
C/Experimental source: BAC clone B14D6; strain OR74A
C/Genetics:

```

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A:Gene: NCSP:B14D6.30
A:Map position: 6
A:Introns: 58/1; 166/1; 267/3; 1543/3

Query Match
Best Local Similarity 27.1%; Score 68; DB 2; Length 1742;
Matches 15; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY 7 QOKYORLLHEVOELTTEVEKIKTTVESATEBEKLTPLVLAK 47
DB 950 EKHQETLDMVEELKTBIAKQALSVESISRTSPVIRRK 990

RESULT 3
S16129
dynein-associated protein, 150K, cytosolic - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S16129
R:Holzbaur, E.L.F.; Hammarback, J.A.; Paschal, B.M.; Kravitz, N.G.; Pfeiffer, K.K.; Vallboe
Native 351, 579-581, 1991
A>Title: Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophila
A:Reference number: S16129; MUID:91260877; PMID:1828535
A:Accession: S16129
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1325 <KTV>
A:Cross-references: UNIPROT:P28023

Query Match
Best Local Similarity 26.9%; Score 67.5; DB 2; Length 1325;
Matches 17; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

OY 1 GVKETPOOKYORLLHEVOELTTEVEKIKTTVESATEBEKLTPLVLAK 49
DB 314 GAESLQGEVEALKERVDLITLDELKALKEKSGSDAASVQL-KQL 361

RESULT 4
T22235
hypochemical protein P45G2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22235
R:Lindsay, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19535
A:Accession: T22235
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1287 <WTL>
A:Cross-references: UNIPROT:062245; EMBL:Z93382; PIDN:CAB07612.1; GSPDB:GN00021; CESP:F
A:Experimental source: clone P45G2
C:Genetics:
A:Gene: CESP:P45G2.3
A:Map position: 3
A:Introns: 59/2; 117/3; 153/3; 180/2; 233/2; 341/3; 393/1; 424/2; 551/3; 664/3; 734/3; 8

Query Match
Best Local Similarity 26.7%; Score 67; DB 2; Length 1287;
Matches 18; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

OY 4 ETPOOKYORLLHEVOELTTEV-EKIKTTVESATEBEKLTPLVLAK 50
DB 1122 EPPPEKQKILIEVIDDPSFFQEKVKENTKESVAEKEVNSNEBKPPILKRAVS 1178

RESULT 5
D90011
Futb protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D90011

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[illegible]

Best Local Similarity 36.4%; Pred. No. 50;
Matches 20; Conservative 10; Mismatches 21; Indels 4; Gaps 2;
QY 1 GVKETPQOKYORLLH---VOELTEVEKIKTTVESATEEKLTPVLLAKQIAL 52
Db 188 GVGCGGPKAKAALKEFQSVELVANTRERLSGKTQMIQEDQKET-TLLSKRLATL 241

RESULT 8
T41023
probable nuclear pore complex-associated protein - fission yeast (Schizosaccharomyces po
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41023
R/Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, June 1998
A/Reference number: 221965
A/Accession: T41023
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1837 <MUR>
A/Cross-references: UNIPROT:O74424; EMBL:AL023860; PIDN:CAA19588.1; GSPDB:GN00068; SPDB:
C/Genetics:
A/Experimental source: strain 972h-; cosmid c162
A/Map position: 3

Query Match 26.1%; Score 65.5; DB 2; Length 1837;
Best Local Similarity 35.8%; Pred. No. 1.3e+02;
Matches 19; Conservative 10; Mismatches 17; Indels 7; Gaps 2;
QY 7 QOKYORLLHVOELTEVEKIKTTV--KESATEEKLTPVLLAK-----QLAAL 52
Db 662 QTSYQSRSLRLEQLTNELESKISRNKKEFEALISLQLEKSNIGQLTSL 714

RESULT 9
E84499
hypothetical protein At2g11890 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004
C/Accession: E84499
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Unayam, L.; Tallon, L.
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: E84499
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-210 <STO>
A/Cross-references: UNIPROT:Q9S1Y3; GB:AE002093; NID:g4557062; PIDN:AA022501.1; GSPDB:GN
C/Genetics:
A/Gene: At2g11890
A/Map position: 2
C/Superfamily: uncharacterized CYTH domain protein

Query Match 25.5%; Score 64; DB 2; Length 210;
Best Local Similarity 40.5%; Pred. No. 17;
Matches 17; Conservative 9; Mismatches 14; Indels 2; Gaps 2;
QY 1 GVK-ETPQOKYOR-RLHVEOELTEVEKIKTTVESATEEKL 40
Db 150 GVKLEVDETKYDFGNCVYIECBETEPERVKTMIEEFLTEEKL 191

RESULT 10
S69518
hypothetical protein 12 - phage HPI
C/Species: phage HPI
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S69518

R.Exposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scoocca,
Nucleic Acids Res. 24, 2360-2368, 1996
A/Title: The complete nucleotide sequence of bacteriophage HPI DNA.
A/Reference number: S69503; MUID:96279738; PMID:8710508
A/Accession: S69518
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-163 <ESP>
A/Cross-references: UNIPROT:P51714; EMBL:U24159; NID:g1046235; PIDN:AA09197.1; PID:g104
C/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C/Superfamily: phage HPI hypothetical protein 12

Query Match 25.3%; Score 63.5; DB 2; Length 163;
Best Local Similarity 37.8%; Pred. No. 15;
Matches 17; Conservative 11; Mismatches 16; Indels 1; Gaps 1;
QY 5 TPQOKYORLLHVOELTEVEKIK--TTVESATEEKLTPVLLAKQ 48
Db 25 TPQOKYORLLHVEFGLCSGVAKKPDVTKDSIGDCTVAVILAKQ 69

RESULT 11
D70391
hypothetical protein aq_1060 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: D70391
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: D70391
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-374 <AOP>
A/Cross-references: UNIPROT:O67159; GB:AE000721; NID:g2983544; PIDN:AA07129.1; PID:g298
A/Experimental source: strain VFS
C/Genetics:
A/Gene: aq_1060
C/Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

Query Match 25.3%; Score 63.5; DB 2; Length 374;
Best Local Similarity 31.1%; Pred. No. 36;
Matches 19; Conservative 14; Mismatches 13; Indels 15; Gaps 3;
QY 6 PQOKYOR-----LHVE-----VOELTEVEKIKTTVESATEEKLTPVLLAKQIAL 51
Db 164 PRRFEEVDNMLKVLHREYLEKSIQEIINTEIRAKKGI-ENARNEKTEIEELKEELSS 222

QY 52 L 52
Db 223 L 223

RESULT 12
F75216
hypothetical protein PAB2181 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: F75216
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A/Reference number: A75001
A/Accession: F75216
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-281 <KAM>
A/Cross-references: UNIPROT:Q9V217; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB4918
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: PAB2181

Query Match 25.1%; Score 63; DB 2; Length 281;
 Best Local Similarity 36.6%; Pred. No. 30;
 Matches 15; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

Qy 1 GVKE-TPQOKYQRLHVEQLTTEVEKIKTVKESATEEKL 40
 Db 119 GIKEVVAEEYKELKKEVEKIKQEFEEVAKI-EAAHEESL 158

RESULT 13

P90577
 lipoprotein vaaB [imported] - Mycoplasma pulmonis (strain UAB CTIP) (fragment)

C/Species: Mycoplasma pulmonis
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: P90577
 R/Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001
 A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult

A/Reference number: A99512; MUID:21267165; PMID:11353084
 A/Accession: P90577

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-314 <KUR>
 A/Cross-references: UNIPROT:Q98Q43; GB:AL445566; PID:g14089940; PIDN:CAC13699.1; GSPDB:G

A/Experimental source: strain UAB CTIP
 C/Genetics:

A/Map position: 5
 A/Genetic code: SGC3

Query Match 25.1%; Score 63; DB 2; Length 314;
 Best Local Similarity 29.8%; Pred. No. 34;
 Matches 14; Conservative 17; Mismatches 10; Indels 6; Gaps 2;

Qy 2 VKETPOQKYQRLHVEQLTTEVEKIKTVKESATEEKLTPVL 44
 Db 246 ITBEOKAKFKDVIQDARTKQDLTKLEKIKS-EKENIEKKLDPII 290

RESULT 14

UC5368

dynactin 1 - mouse

N/Alternate names: p150 Glued
 C/Species: Mus musculus (house mouse)

C/Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
 C/Accession: J05368

R/Jiang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
 Biochem. Biophys. Res. Commun. 231, 344-347, 1997

A/Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th
 A/Reference number: J05368; MUID:97223454; PMID:9070275

A/Accession: J05368
 A/Molecule type: mRNA

A/Residues: 1-1281 <UN>
 A/Cross-references: UNIPROT:O08788; GB:U60312; NID:G2104494; PIDN:AAB5773.1; PID:G21044

A/Experimental source: brain
 C/Comment: This protein is a member of the oligomeric dynactin complex that is required

C/Genetics:
 A/Map position: 6

Query Match 24.9%; Score 62.5; DB 2; Length 1281;
 Best Local Similarity 34.8%; Pred. No. 1.8e+02;
 Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Qy 4 ETPOQKYQRLHVEQLTTEVEKIKTVKESATEEKLTPVLIQKL 49
 Db 319 ESLQOEVALKERVDELTTDLITLKAIEKSGDGAASYQL-KQL 363

RESULT 15

T32222
 hypochetrical protein T23B12.7 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32222
 R/Davidson, S.; Wohldmann, P.; Gillam, B.

submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid T23B12.

A/Reference number: Z21137
 A/Accession: T32222

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-296 <DAV>
 A/Cross-references: UNIPROT:Q17002; EMBL:AF022982; PIDN:AAB69938.1; GSPDB:GN00023; CESP:

A/Experimental source: strain Bristol N2; clone T23B12
 C/Genetics:

A/Map position: 5
 A/Introns: 67/3

Query Match 24.7%; Score 62; DB 2; Length 296;
 Best Local Similarity 31.0%; Pred. No. 40;
 Matches 18; Conservative 12; Mismatches 12; Indels 16; Gaps 3;

Qy 3 KETPOQKYQRLHVEQLTTEVEKIKTVKESATEEKLTPVLIQKL 47
 Db 132 KKTQQRNFK--ESIEAIRQLERKRVNEEVKQKATLTKTEREKIKQSOEKLTPRLILK 186

Search completed: November 3, 2005, 22:04:16
 Job time : 18.9091 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 3, 2005, 21:51:39 ; Search time 15.4011 Seconds

(without alignments)
145.410 Million cell updates/sec

Title: 09782816-1-22

Perfect score: 138

Sequence: 1 EVKIKTTVKESATEEKLTPVLLAKQIAL 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiletest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	37.0	136	4	US-09-270-767-36154
2	51	37.0	136	4	US-09-270-767-51371
3	50	36.2	938	4	US-09-637-145-2
4	49.5	35.9	119	4	US-09-621-976-4332
5	49.5	35.5	413	4	US-09-107-532A-6433
6	49	35.5	1027	4	US-09-107-532A-6675
7	48.5	35.1	124	4	US-09-513-999C-6026
8	48.5	35.1	280	3	US-09-470-512A-14
9	48.5	35.1	451	4	US-09-270-767-45139
10	48	34.8	1200	4	US-09-107-532A-6432
11	48	34.8	1428	4	US-09-644-827B-7
12	48	34.8	167	4	US-09-644-827B-7
13	47.5	34.4	314	4	US-09-166-350-13
14	47.5	34.4	314	4	US-09-902-540-16180
15	47.5	34.4	403	4	US-09-976-594-421
16	47	34.1	103	4	US-09-732-210-1198
17	47	34.1	180	4	US-09-648-004-2
18	47	34.1	180	4	US-10-272-419-2
19	47	34.1	289	4	US-09-071-035-480
20	47	34.1	317	3	US-09-134-001C-3712
21	47	34.1	387	4	US-09-248-796A-1845
22	47	34.1	424	4	US-09-286-981B-14
23	47	34.1	425	4	US-09-286-981B-13
24	47	34.1	426	4	US-09-286-981B-12
25	47	34.1	450	4	US-09-071-035-256
26	47	34.1	708	4	US-09-134-000C-5994
27	47	34.1	894	4	US-09-071-035-248

28	47	34.1	940	4	US-09-328-352-8165	Sequence 8165, Ap
29	47	34.1	962	4	US-09-071-035-246	Sequence 246, App
30	47	34.1	962	4	US-09-071-035-250	Sequence 250, App
31	47	34.1	962	4	US-09-071-035-254	Sequence 254, App
32	47	34.1	962	4	US-09-071-035-470	Sequence 470, App
33	47	34.1	962	4	US-09-071-035-474	Sequence 474, App
34	47	34.1	962	4	US-09-071-035-478	Sequence 478, App
35	47	34.1	970	4	US-09-134-000C-5691	Sequence 5691, Ap
36	46.5	33.7	1964	3	US-09-467-997-1	Sequence 1, Appl
37	46	33.3	192	4	US-09-248-796A-20678	Sequence 20678, A
38	46	33.3	366	4	US-09-134-000C-4956	Sequence 4956, Ap
39	46	33.3	757	3	US-08-434-000A-6	Sequence 6, Appl
40	46	33.3	757	3	US-09-312-157-6	Sequence 6, Appl
41	46	33.3	757	3	US-09-717-888-6	Sequence 6, Appl
42	46	33.3	1896	4	US-09-949-016-9508	Sequence 9508, Ap
43	46	32.6	103	4	US-09-732-210-1119	Sequence 1119, Ap
44	45	32.6	103	4	US-09-286-981B-1	Sequence 1, Appl
45	45	32.6	114	4	US-09-286-981B-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-09-270-767-36154
; Sequence 36154, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36154
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-51371

Query Match      37.0%; Score 51; DB 4; Length 136;
Best Local Similarity 40.0%; Pred. No. 7.6;
Matches 14; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

Cy      2 VEKIKTT-----VKESATEEKLTPVLLAKQIAL 30
Db      37 IDKIKTTPTANPKTKRPTSNMKLSAVLLATALLAL 71

RESULT 2
US-09-270-767-51371
; Sequence 51371, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51371
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-51371

Query Match      37.0%; Score 51; DB 4; Length 136;
Best Local Similarity 40.0%; Pred. No. 7.6;
Matches 14; Conservative 6; Mismatches 9; Indels 6; Gaps 1;
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Db 37 IDKVTPTANPKTKPTSNMKTSAVLALIALIAL 71

RESULT 3
US-09-637-145-2
; Sequence 2, Application US/09637145
; Patent No. 6673587
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: KAO, HUNG-YING
; APPLICANT: DOMNES, MICHAEL
; APPLICANT: ORDENTLICH, PETER
; TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR
; FILE REFERENCE: SAL3000
; CURRENT APPLICATION NUMBER: US/09/637,145
; CURRENT FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-637-145-2

Query Match 36.2%; Score 50; DB 4; Length 938;
Best Local Similarity 44.0%; Pred. No. 94;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 6 KTVKESATEKLTPTVLAKQAL 30
Db 100 RSAVSSVVKOKLAELVILKKQOAL 124

RESULT 4
US-09-621-976-4332
; Sequence 4332, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4332
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 66
; OTHER INFORMATION: Xaa = *, Trp
US-09-621-976-4332

Query Match 35.9%; Score 49.5; DB 4; Length 119;
Best Local Similarity 40.6%; Pred. No. 11;
Matches 13; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

OY 1 EVEKIKTVKESATEKLTPTVLAKQ--LAA 29
Db 62 ELDKKTITMKSSVQECVSTISSKDEDPPLAA 93

RESULT 5
US-09-107-532A-6433
; Sequence 6433, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS: GENOME THERAPEUTICS CORPORATION
ADDRESS: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6433:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...413
SEQUENCE DESCRIPTION: SEQ ID NO: 6433:
US-09-107-532A-6433

Query Match 35.5%; Score 49; DB 4; Length 413;
Best Local Similarity 44.4%; Pred. No. 51;
Matches 12; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 1 EVEKIKTVKESATEKLTPT--VLAK 25
Db 64 EERSQTAVALTKENRLTRGGVLT 90

RESULT 6
US-09-107-532A-6675
; Sequence 6675, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC

OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
TELEPHONE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6675:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1027
SEQUENCE DESCRIPTION: SEQ ID NO: 6675:
US-09-107-532A-6675

Query Match 35.5%; Score 49; DB 4; Length 1027;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 EVEKITVKSATEEKLTP--VLAK 25
Db 788 EERSQTAVVELTKENRLTPGVVLT 814

RESULT 7
US-09-513-999C-6026
Sequence 6026, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6026
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 46
OTHER INFORMATION: Xaa-Gln or Arg
US-09-513-999C-6026

Query Match 35.1%; Score 48.5; DB 4; Length 124;
Best Local Similarity 39.3%; Pred. No. 15;
Matches 11; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
Qy 1 EVEKITVKSATE-EKLTPLVLAKOL 27

Db 40 EEKVKKSVADAKKGQKDVCTVLAKEM 67

RESULT 8
US-09-470-512A-14
Sequence 14, Application US/09470512A
Patent No. 6378652
GENERAL INFORMATION:
APPLICANT: PhageTech, Inc.
TITLE OF INVENTION: Compositions and methods involving an essential Staphylococcus Au
FILE REFERENCE: 21715/1000
CURRENT APPLICATION NUMBER: US/09/470,512A
CURRENT FILING DATE: 1999-12-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 280
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-470-512A-14

Query Match 35.1%; Score 48.5; DB 3; Length 280;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 11; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

Qy 2 VEKITVKSATEEKL-----TPVLAKQDA 29
Db 171 VRELKNSLDQTLERKLNMTTTPVLMDDIGA 203

RESULT 9
US-09-270-767-45139
Sequence 45139, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homberger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45139
LENGTH: 451
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45139

Query Match 35.1%; Score 48.5; DB 4; Length 451;
Best Local Similarity 39.3%; Pred. No. 67;
Matches 11; Conservative 11; Mismatches 5; Indels 1; Gaps 1;

Qy 1 EVEKITVKSATE-EKLTPLVLAKOL 27
Db 79 EEKVKKSLKQAQAKNDRTCVILAKEL 106

RESULT 10
US-09-107-532A-6432
Sequence 6432, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSES:
ADDRESSER: GENOM THERAPEUTICS CORPORATION
STREET: 100 Beaver Street

```

; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8) LOCATION 1...107
; SEQUENCE DESCRIPTION: SEQ ID NO: 6432:
US-09-107-532A-6432

Query Match 34.8%; Score 48; DB 4; Length 107;
Best Local Similarity 47.6%; Pred. No. 15;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 5 IKTVKESATEKLTPLVLAK 25
:|::|||:|
Db 84 LKNIVSKNIEIKTIPVQDK 104

RESULT 11
US-09-644-827B-8
; Sequence 8, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caspase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644,827B
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-8

Query Match 34.8%; Score 48; DB 4; Length 1200;
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; Best Local Similarity 42.3%; Pred. No. 2.4e+02;
; Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 5 IKTVKESATEKLTPLVLAKQAL 30
:|::|||:|
Db 148 VACAVASSVVKLAELVILKKQNAL 173

RESULT 12
US-09-644-827B-7
; Sequence 7, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caspase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644,827B
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-7

Query Match 34.8%; Score 48; DB 4; Length 1428;
Best Local Similarity 42.3%; Pred. No. 2.9e+02;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 5 IKTVKESATEKLTPLVLAKQAL 30
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Db 374 VACAVASSVVKLAELVILKKQNAL 399

RESULT 13
US-09-166-350-13
; Sequence 13, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockett, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-13

Query Match 34.4%; Score 47.5; DB 4; Length 167;
Best Local Similarity 40.6%; Pred. No. 30;
Matches 13; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 1 EKKIKTVKESATEKLTPLVLAKQ--LAA 29
:|::|||:|
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Db 100 ELDKWTMKSSVQECVSTISSKEDDPLAA 131

RESULT 14

US-09-902-540-16180
; Sequence 16180, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15869)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16180
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16180

Query Match 34.4%; Score 47.5; DB 4; Length 314;

Best Local Similarity 50.0%; Pred. No. 61;
Matches 13; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 3 EKIKTVESATEEKLTP-VILAKQL 27

Db 244 EALKTFVEKATKRVTSVVLNPL 269

RESULT 15

US-09-976-594-421
; Sequence 421, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 421
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1756951CD1
US-09-976-594-421

Query Match 34.4%; Score 47.5; DB 4; Length 403;

Best Local Similarity 40.6%; Pred. No. 81;
Matches 13; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 1 EFKIKTVESATEEKLTPVILAKQ--LAA 29

Db 62 ELDKWTMKSSVQECVSTISSKEDDPLAA 93

Search completed: November 3, 2005, 22:05:55
Job time : 16.4011 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:53:15 ; Search time 54.0642 Seconds
(without alignments)
232.174 Million cell updates/sec

Title: 09782816-1-22

Perfect score: 138
Sequence: 1 EVEKIKTVKESATEEKLTPVLAKQIAL 30

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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12: /cgn2_6/prodata/1/pubppa/US09D_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
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22: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	134	14	US-10-106-698-6730 Sequence 6730, Ap
2	138	100.0	401	16	US-10-408-765A-1369 Sequence 1369, Ap
3	138	100.0	406	10	US-09-782-816A-53 Sequence 53, Appl
4	138	100.0	465	9	US-09-925-298-676 Sequence 676, App
5	138	100.0	465	14	US-10-102-806-676 Sequence 676, App
6	135	97.8	183	10	US-09-782-816A-54 Sequence 54, Appl
7	135	97.8	224	16	US-10-425-115-315831 Sequence 315831, Appl
8	133	96.4	52	10	US-09-782-816A-51 Sequence 51, Appl
9	103	74.6	23	10	US-09-782-816A-1 Sequence 1, Appl
10	56	40.6	334	18	US-10-501-282-4734 Sequence 4734, Ap
11	51	37.0	447	15	US-10-335-977-7239 Sequence 7239, Ap

12	51	37.0	773	15	US-10-335-977-7240 Sequence 7240, Ap
13	51	37.0	932	15	US-10-282-122A-47253 Sequence 47253, A
14	51	37.0	10917	17	US-10-732-923-20606 Sequence 20606, A
15	50	36.2	211	16	US-10-425-115-212374 Sequence 212374, A
16	50	36.2	640	15	US-10-282-122A-44691 Sequence 44691, A
17	50	36.2	773	9	US-09-815-242-11330 Sequence 11330, A
18	50	36.2	773	15	US-10-282-122A-58722 Sequence 58722, A
19	50	36.2	855	9	US-09-817-913-13 Sequence 13, Appl
20	50	36.2	855	14	US-10-172-094-9 Sequence 9, Appl
21	50	36.2	855	15	US-10-189-818B-4 Sequence 4, Appl
22	50	36.2	855	16	US-10-870-587-13 Sequence 13, Appl
23	50	36.2	902	16	US-10-437-963-105564 Sequence 105564, A
24	50	36.2	902	16	US-09-800-187-12 Sequence 12, Appl
25	50	36.2	912	10	US-10-175-559-2 Sequence 2, Appl
26	50	36.2	915	14	US-10-087-192-1893 Sequence 1893, Ap
27	50	36.2	952	15	US-10-741-600-1176 Sequence 7, Appl
28	50	36.2	952	15	US-10-360-534-7 Sequence 1176, Ap
29	50	36.2	1642	17	US-10-741-600-1178 Sequence 1178, Ap
30	50	36.2	1642	17	US-10-408-765A-1977 Sequence 1977, Ap
31	50	36.2	3024	16	US-10-788-792-1170 Sequence 1170, App
32	50	36.2	3396	17	US-10-741-600-1172 Sequence 1172, Ap
33	50	36.2	3396	17	US-10-741-600-1173 Sequence 1173, Ap
34	50	36.2	3396	18	US-10-631-467-773 Sequence 773, App
35	50	36.2	387	9	US-09-864-761-43703 Sequence 43703, A
36	49	35.5	279	15	US-10-282-122A-57857 Sequence 57857, A
37	49	35.5	291	16	US-10-767-701-40287 Sequence 40287, A
38	49	35.5	307	11	US-09-972-211-73 Sequence 73, Appl
39	49	35.5	307	15	US-10-096-625-73 Sequence 73, Appl
40	49	35.5	307	15	US-09-972-211-72 Sequence 72, Appl
41	49	35.5	340	11	US-10-096-625-72 Sequence 72, Appl
42	49	35.5	340	15	US-10-723-860-1930 Sequence 1930, Ap
43	49	35.5	340	16	US-10-756-149-5208 Sequence 5208, Ap
44	49	35.5	340	18	US-10-450-763-52703 Sequence 52703, A
45	49	35.5	352	18	

ALIGNMENTS

RESULT 1
US-10-106-698-6730
; Sequence 6730, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: P000591
; CURRENT APPLICATION NUMBER: US/10/106,698
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6730
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6730

Query Match 100.0%; Score 138; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVEKIKTVKESATEEKLTPVLAKQIAL 30
|||||

Db 19 EVEKITTVKESATEEKLTPVLAQKQAL 48

RESULT 2

US-10-408-765A-1369
; Sequence 1369, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bohn D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1369
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1369

Query Match 100.0%; Score 138; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEKITTVKESATEEKLTPVLAQKQAL 30
Db 116 EVEKITTVKESATEEKLTPVLAQKQAL 145

RESULT 3

US-09-782-816A-53
; Sequence 53, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069.001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-816A-53

Query Match 100.0%; Score 138; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEKITTVKESATEEKLTPVLAQKQAL 30
Db 121 EVEKITTVKESATEEKLTPVLAQKQAL 150

RESULT 4

US-09-925-298-676
; Sequence 676, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103

; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-676

Query Match 100.0%; Score 138; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEKITTVKESATEEKLTPVLAQKQAL 30
Db 180 EVEKITTVKESATEEKLTPVLAQKQAL 209

RESULT 5

US-10-102-806-676
; Sequence 676, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURES:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-676

Query Match 100.0%; Score 138; DB 14; Length 465;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEKIKTVKESATEEKTLPVLLAKQLAAL 30
 |||||
Db 180 EVEKIKTVKESAETEEKTLPVLLAKQLAAL 209

```

RESULT 6
US-09-782-816A-54
; Sequence 54, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Schooley, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069, 001A
; CURRENT APPLICATION NUMBER: US/09/782, 816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRP
; ORGANISM: Mus musculus
US-09-782-816A-54

```

Query Match	97.8%	Score 135;	DB 10;	Length 183;
Best Local Similarity	96.7%	Pred. No. 8.7e-11;		
Matches 29;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 EVEKIKITVKSATTEEKLTPVLAKQLAAL 30  
        |||||  
Db      116 EVEKIKITVKSATTEEKLTPVLAKQLAAL 145
```

RESULT 7
 US-10-425-115-315831
 ; Sequence 315831, Application US/10425115
 ; Publication NO. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 315831
 ; LENGTH: 224
 ; TYPE: PR1
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_51109C.1.pep
 ; US-10-425-115-315831

Query Match	97.8%	Score 135;	DB 16;	Length 224;
Best Local Similarity	96.7%	Pred. No. 1.1e-10;		
Matches 29;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 EVEKIKTTVESATEEKLTPVLAKQALAL 30
        |||||:|||||
Db      69 EVEKIKTTVESATEEKLTPVLAKQALAL 98
```

RESULT 8
US-09-782-816A-51
; Sequence 51, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.

```

? APPLICANT: Rogers, Gregory C.
? APPLICANT: Scholey, Jonathan M.
? TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
? TITLE OF INVENTION: PROLIFERATION
? FILE REFERENCE: UC069,001A
? CURRENT APPLICATION NUMBER: US/09/782,816A
? CURRENT FILING DATE: 2001-02-14
? NUMBER OF SEQ. ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 51
? LENGTH: 52
? TYPE: PRT
? ORGANISM: Unknown
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: 44
? OTHER INFORMATION: Xaa = Val or Leu
? OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
? US-09-782-816A-51

```

Query Match	96.4%	Score 133;	DB 10;	Length 52;
Best Local Similarity	96.7%	Pred. No. 3.8e-11;		
Matches 29; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1 EYEKIKTVESATEEKLTPVLAKQIAL 30
        |||||
Db       23 EVEKIKTVESATEEKLTPVXLAKQIAL 52
```

```

RESULT 9
US-09-782-816A-1
; Sequence 1, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069,001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ. ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa = Val or Leu
; OTHER INFORMATION: The sequence is a Homo sapiens sequence when Xaa
; OTHER INFORMATION: represents Leu and a Mus musculus sequence when.
; OTHER INFORMATION: Xaa represents Val.
US-09-782-816A-1

```

Query Match	74.6%	Score 103;	DB 10;	Length 23;
Best Local Similarity	95.7%	Pred. No. 2.3e-07;		
Matches	22;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

```
QY      1 EVEKIKITVKESATEEKLTPVLL 23  
        |||||  
Db      1 EVEKIKITVKESATEEKLTPVXL 23
```

RESULT 10
US-10-501-282-4734
; Sequence 4734, Application US/10501282;
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN

APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOTOCOCUS OTTITIS OPEN READING FRAMES (ORFS) ENCODING
FILE REFERENCE: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
CURRENT FILING DATE: 2004-07-09
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4734
LENGTH: 334
TYPE: PRT
ORGANISM: *Alloccoccus otitidis*
US-10-501-282-4734

Query Match 40.6%; Score 56; DB 18; Length 334;
Best Local Similarity 34.5%; Pred. No. 21;
Matches 10; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Cy 2 VEXIKTKSATEKLTPLVLAQKQL 30
Db 244 IDQIKSTIKSGSVKTKLGLIKKQLSSL 272

RESULT 11

US-10-335-977-7239
Sequence 7239, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7239:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

ORIGINAL SOURCE:
ORGANISM: *Helicobacter pylori*
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...447
SEQUENCE DESCRIPTION: SEQ ID NO: 7239:
US-10-335-977-7239

Query Match 37.0%; Score 51; DB 15; Length 447;
Best Local Similarity 43.5%; Pred. No. 1.5e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 5 IKTVKESATEKLTPLVLAQKQL 27
Db 202 LKQFVKDSAKKELTPIIAFRSM 224

RESULT 12

US-10-335-977-7240
Sequence 7240, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7240:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: *Helicobacter pylori*
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...773
SEQUENCE DESCRIPTION: SEQ ID NO: 7240:
US-10-335-977-7240

Query Match 37.0%; Score 51; DB 15; Length 773;
Best Local Similarity 43.5%; Pred. No. 2.8e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 5 IKTVKESATEKLTPLVLAQKQL 27
Db 202 LKQFVKDSAKKELTPIIAFRSM 224

Db 222 LKQFVKSATKELTPVLAQAL 244

RESULT 13

US-10-282-122A-47253
; Sequence 47253, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykend, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Cart, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

CURRENT FILING DATE: 2003-02-20
CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16
Remainder of prior application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1

SEQ ID NO 47253
LENGTH: 932

TYPE: PRT
ORGANISM: Borrelia burgdorferi

US-10-282-122A-47253

Query Match 37.0%; Score 51; DB 15; Length 932;
Best Local Similarity 37.9%; Pred. No. 3.5e+02;
Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 VEKIKTVKSATKELTPVLAQAL 30
Db 397 IDKIDKATKEIYIKNKLTPLKIAQPEGAM 425

RESULT 14

US-10-732-923-20606
; Sequence 20606, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52796)C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 20606
; LENGTH: 10917
; TYPE: PRT
; ORGANISM: Streptomyces nodosus
US-10-732-923-20606

Query Match 37.0%; Score 51; DB 17; Length 10917;
Best Local Similarity 46.2%; Pred. No. 6.4e+03;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 IKTVKSATKELTPVLAQAL 30
Db 1633 IRTVRRRAAGVSVTADGLAQALGL 1658

RESULT 15

US-10-425-115-212374
; Sequence 212374, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yinhua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 212374
LENGTH: 211

TYPE: PRT

ORGANISM: Zea mays

OTHER INFORMATION: Clone ID: MRT4577_125287C.1.pcp

US-10-425-115-212374

Query Match 36.2%; Score 50; DB 16; Length 211;
Best Local Similarity 53.6%; Pred. No. 84;
Matches 15; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 1 EVEKIKTVKSATKELTPVLAQAL 28
Db 97 ELEKAKTVEELT-KLDVYVNSKOLA 122

Search completed: November 3, 2005, 22:11:39
Job time: 56.0642 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 3, 2005, 21:32:33 ; Search time 71.1872 Seconds
(without alignments)
282.516 Million cell updates/sec

Title: 09782816-3-1-22

Sequence: 1 GKETPQOKTQRLHVEQL.....ESATEKLTPLYLAKQLAAL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	100.0	314	8	ABM81421 Tumour-as
2	251	100.0	378	6	ABP98851 Human str
3	251	100.0	401	7	ADJ69563 Human hea
4	251	100.0	406	5	ABP53018 Human p50
5	251	100.0	465	3	ABBS8968 Breast an
6	248	98.8	183	5	ABP53019 Mouse p50
7	246	98.0	52	5	ABP53016 Cellular
8	231	92.0	134	4	AAg75956 Human col
9	113	45.0	22	5	ABP52968 Cellular
10	107	42.6	21	5	ABP52969 Cellular
11	103	41.0	20	5	ABP52970 Cellular
12	103	41.0	23	5	ABP52966 Cellular
13	98	39.0	19	5	ABP52971 Cellular
14	93	37.1	18	5	ABP52972 Cellular
15	88	35.1	17	5	ABP52973 Cellular
16	81	32.3	16	5	ABP52974 Cellular
17	76	30.3	15	5	ABP52975 Cellular
18	72.5	28.9	53	5	ABP53017 Cellular
19	72.5	28.9	380	5	ABBS9088 Drosophi
20	72.5	28.9	380	5	ABP53020 Drosophi
21	71	28.3	14	5	ABP52976 Cellular
22	70	27.9	1087	4	ABBS6539 Drosophi
23	70	27.9	1087	4	ABBS6538 Drosophi
24	68	27.1	2368	4	AAU34139 Staphyloc
25	68	27.1	2368	4	AAU36796 Staphyloc

26	67	26.7	1448	6	ADA89551 Staphyloc
27	67	26.7	2478	4	AAU37374 Staphyloc
28	67	26.7	2478	4	AAU34320 Staphyloc
29	67	26.7	2478	6	ABJ19002 Pathogen
30	67	26.7	2478	6	ABM71899 Staphyloc
31	67	26.7	2481	6	ABU15838 Protein e
32	67	26.7	2481	7	ABR62804 Methicill
33	66	26.3	13	5	ABP52977 Cellular
34	66	26.3	386	6	ABU44043 Protein e
35	66	26.3	868	2	AAV37731 Protein i
36	66	26.3	1020	4	AAW79875 Human pro
37	65.5	26.1	207	4	AAAB29754 Rice pNf-
38	65.5	26.1	1837	8	ADA44304 Bacteri
39	64	25.5	140	4	AAO12168 Human pol
40	64	25.5	151	3	AAQ03725 Human sec
41	64	25.5	188	2	AAW64545 Human sco
42	64	25.5	188	3	AAU10278 Human fet
43	64	25.5	188	4	AAU12172 Human PRO
44	64	25.5	188	6	ABO17616 Novel hum
45	64	25.5	188	6	ABU80870 Human PRO

ALIGNMENTS

RESULT 1	ABM81421 standard; protein; 314 AA.
XX	ABM81421;
XX	AC
XX	18-NOV-2004 (first entry)
XX	DT
XX	DE
XX	Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ.3675.
XX	KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX	KW tumour; diagnosis; cell proliferative disorder; breast cancer;
XX	KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX	KW central nervous system cancer; bladder cancer; pancreatic cancer;
XX	KW cervical cancer; melanoma; leukaemia; hybridisation probe;
XX	KW chromosome identification; chromosome mapping; gene mapping;
XX	KW gene therapy; cytostatic.
OS	Homo sapiens.
XX	WO2004030615-A2.
XX	15-APR-2004.
XX	29-SEP-2003; 2003WO-US028547.
XX	PR 02-OCT-2002; 2002US-0414971P.
XX	PA (GETH) GENENTECH INC.
XX	PI Wu TD, Zhang Z, Zhou Y;
XX	DR WPI; 2004-347921/32.
XX	PT N-PSDB; ACN39497.
XX	PT New tumor-associated antigenic target polypeptides and nucleic acids,
XX	PT useful in preparing a medicament for treating or detecting a
XX	PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX	PT prostate cancer or tumor.
XX	PS Claim 12; SEQ ID NO 3675; 7273bp; English.
XX	CC The invention relates to human tumour-associated antigenic target (TAT)
XX	CC polypeptides, and their related nucleic acids. The TAT polypeptides are
XX	CC overexpressed in cancer tissues compared to normal tissues, and may thus
XX	CC serve as effective targets for the diagnosis and treatment of cancer in
XX	CC mammals. The invention also relates to nucleic acid and polypeptide
XX	CC sequences at least 80% identical to the TAT nucleic acid and

CC polypeptides; expression vectors and host cells comprising a TAR nucleic acid; an antibody specific for a TAR polypeptide; a peptide or organic molecule which binds to a TAR polypeptide; fusion proteins comprising a TAR polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAR polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAR expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAR nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAR polypeptide of the invention

SO Sequence 314 AA;

Query Match 100.0%; Score 251; DB 8; Length 314;
Best Local Similarity 100.0%; Pred. No. 6e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYORLHVEQELTTEVEKIKTKTKESATREKTPVLLAKQALAL 52
DB 7 GVKETPOOKYORLHVEQELTTEVEKIKTKTKESATREKTPVLLAKQALAL 58

RESULT 2
ABP98851
ID ABP98851 standard; protein; 378 AA.
AC ABP98851;
XX
XX 15-JUN-2003 (first entry)
DT
XX
DE Human structural and cytoskeletal associated protein #42.
XX
XX Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal;
KW neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic;
KW antiinflammatory; antiarthritic; vinicide; gene therapy; human; stroke;
KW structural and cytoskeleton-associated protein; SCAP; cancer; angina;
KW atherosclerosis; epilepsy; Huntington's disease; hypertension;
KW heart failure; osteoporosis; osteoarthritis.
XX
XX Homo sapiens.
OS
XX W02003031940-A2.
PN
XX 17-APR-2003.
PD
XX
XX 10-OCT-2002; 2002WO-US032851.
PF
XX 12-OCT-2001; 2001US-0328931P.
PR 19-OCT-2001; 2001US-036081P.
PR 02-NOV-2001; 2001US-0343896P.
PR 09-NOV-2001; 2001US-0346308P.
PR 16-NOV-2001; 2001US-0332385P.
PR 07-DEC-2001; 2001US-0340776P.
PR 11-JAN-2002; 2002US-0347703P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
PI Becha SD, Bhattacharya V, Borowsky MT, Burrill JD, Chang H,
PI Chawla NK, Elliott US, Emerling BM, Forsythe JT, Gorrard AE,
PI Griffin JA, Hafalia AD, Ho A, Ison CH, Kable AE, Khare R, Lal PG,
PI Lee S, Lee EA, Lee SY, Lehr-Mason PM, Li JX, Lindquist EA, Luo W,
PI Marquis JP, Ramkumar J, Richardson TW, Sprague WW, Swarnakar A,
PI Tang YT, Warren BA, Yang J, Yue H, Zebajadian Y, Zheng W;
XX
XX WPI; 2003-403125/38.
DR N-PSDB; ACC44338.
XX
XX New human structural and cytoskeleton-associated proteins (SCAP) useful
PT for diagnosing, treating and preventing diseases or conditions associated

PT with the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
XX
XX Claim 1; Page 298; 361pp; English.
XX
XX This sequence represents a novel isolated human structural and
CC cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and
CC polynucleotides encoding them are useful in diagnosing, treating and
CC preventing diseases or conditions associated with the decreased
CC expression or over expression of SCAP, such as cell proliferative (e.g.
CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and
CC skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral
CC infections. These are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC SCAP. The SCAP or its fragments are useful in screening compounds for
CC effectiveness as agonist or antagonist of the polypeptides, or in
CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to or modulate the activity of the polypeptide. The
CC microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles
XX

SO Sequence 378 AA;

Query Match 100.0%; Score 251; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.4e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYORLHVEQELTTEVEKIKTKTKESATREKTPVLLAKQALAL 52
DB 71 GVKETPOOKYORLHVEQELTTEVEKIKTKTKESATREKTPVLLAKQALAL 122

RESULT 3
ADU65563
ID ADU65563 standard; protein; 401 AA.
XX
XX
AC ADU65563;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human heat mitochondrial protein as a therapeutic target SegIDJ369.
XX
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytoskeletal.
XX
XX Homo sapiens.
OS
XX W02003087768-A2.
PN
XX 23-OCT-2003.
PD
XX
XX 04-APR-2003; 2003WO-US010870.
PF
XX 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,
PI Warnock DE;
XX
XX WPI; 2003-845369/78.
DR
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.
XX
PS Claim 1; SEQ ID NO 1369; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiallergic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 251; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 7.9e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYORLLHVEVQLTTEVEKIKTVKESATBEKLTPLVLAQQLAAL 52
DB 94 GVKETPOOKYORLLHVEVQLTTEVEKIKTVKESATBEKLTPLVLAQQLAAL 145

RESULT 4
ABP53018
ID ABP53018 standard; protein; 406 AA.
XX
AC ABP53018;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human p50 amino acid sequence SEQ ID NO:53.
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glauclular disorder; macropagal disorder; epithelial disorder;
KM stromal disorder; blastocoeic disorder; angiogenic disorder;
KM immunologic disorder.
XX
XX Homo sapiens.
OS
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Disclosure; Fig 1; 55pp; English.
XX
XX The present invention describes an isolated peptide (1) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumours (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macropagal, epithelial, stromal and blastocoeic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents human p50 which is given in the exemplification of the present
CC invention
XX
SQ Sequence 406 AA;

Query Match 100.0%; Score 251; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 8.1e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYORLLHVEVQLTTEVEKIKTVKESATBEKLTPLVLAQQLAAL 52
DB 99 GVKETPOOKYORLLHVEVQLTTEVEKIKTVKESATBEKLTPLVLAQQLAAL 150

RESULT 5
ID AAB58968
XX
XX AAB58968 standard; protein; 465 AA.
XX
XX
XX 27-MAR-2001 (first entry)
XX
XX
XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 676.
XX
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KM neurotropic; neuroprotective; antiviral; antiallergic; hepatocytic;
KM antidiabetic; antiinflammatory; anticulcer; vulnery; anticonvulsant;
KM antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KM Addison's disease; allergy; autoimmune haemolytic anaemia;
KM autoimmune thyroiditis; diabetes mellitus; Cronh's disease;
KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KM cardiovascular disorder; wound healing; neurological disease.
XX
XX Homo sapiens.
OS
XX WO200055173-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005681.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-611515/58.
XX
XX N-PSDB; AAF21871.
XX
XX
XX New human breast and ovarian cancer associated gene sequences and the
XX polypeptides encoded by these genes, useful in the prevention, treatment
XX and diagnosis of cancer, immune disorders, cardiovascular disorders and
XX neurological diseases.
XX
XX Claim 11; Page 1126-1128; 1299pp; English.
XX
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
XX associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic, immunosuppressive, neutrotropic,
CC neuroprotective, antiviral, antiallergic, hepatocytotoxic, antidiabetic;
CC antiinflammatory; antitumor; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemia; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
CC
XX Sequence 465 AA;
SQ

Query Match 100.0%; Score 251; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 9,4e-21;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQRYRLHVEQELTTEVEKIKTYVESATEEKLTPVLAQQLAL 52
Db 158 GVKEPPOQRYRLHVEQELTTEVEKIKTYVESATEEKLTPVLAQQLAL 209

RESULT 6
AAB53019
ID AAB53019 standard; protein, 183 AA.
XX
AC AAB53019;
XX
DT 05-NOV-2002 (first entry)
XX
DE Mouse p50 amino acid sequence SEQ ID NO:54.
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumor; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoeleic disorder; angiogenic disorder;
KM immunologic disorder.
XX
XX Mus musculus.
OS
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Disclosure; Fig 2; 55pp; English.
XX
XX The present invention describes an isolated peptide (1) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in AAB52966 and AAB52967 and can have C-terminal and N-
XX terminal extensions. (1) have cytostatic and antiinflammatory activities

CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents mouse p50 which is given in the exemplification of the present
CC invention
CC
XX Sequence 183 AA;
SQ

Query Match 98.8%; Score 248; DB 5; Length 183;
Best Local Similarity 98.1%; Pred. No. 7,1e-21;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQRYRLHVEQELTTEVEKIKTYVESATEEKLTPVLAQQLAL 52
Db 94 GVKEPPOQRYRLHVEQELTTEVEKIKTYVESATEEKLTPVLAQQLAL 145

RESULT 7
AAB53016
ID AAB53016 standard; peptide, 52 AA.
XX
AC AAB53016;
XX
DT 05-NOV-2002 (first entry)
XX
XX Cellular proliferation peptide inhibitor SEQ ID NO:51.
XX
XX
XX Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumor; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoeleic disorder; angiogenic disorder;
KM immunologic disorder.
XX
XX Homo sapiens.
OS
XX Mus musculus.
OS
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX Misc-difference 44 /label= Leu, Val
XX FT /note= "Leu in humans and Val in Mus musculus"
XX
XX WO200264779-A2.
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX Claim 2; Page 31; 55pp; English.
XX
XX The present invention describes an isolated peptide (1) comprising or

CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and anti-inflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoelec disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a specifically claimed peptide inhibitor of cellular
CC proliferation from the present invention
CC
XX
SQ Sequence 52 AA;
Query March 98.0%; Score 246; DB 5; Length 52;
Best Local Similarity 98.1%; Pred. No. 2.8e-21;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVKETPOOKYQRLHVEVQLTTEVEKIKTYVESATEERLTPVLLAKQALAL 52
Db 1 GVKETPOOKYQRLHVEVQLTTEVEKIKTYVESATEERLTPVLLAKQALAL 52
RESULT 8
AAG75956
ID AAG75956 standard; protein; 134 AA.
XX
XX AAG75956;
XX
DT 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:6720.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 12.
XX
XX Homo sapiens.
XX
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US026524.
XX
XX 29-SEP-1999; 99US-0157137P.
XX
XX 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Ruden SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX
XX DR N-PSDB; AAH35361.
XX
XX Nucleic acid encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX
XX Claim 1; Page 8181; 9803pp; English.
XX
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used

CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication. meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
XX
SQ Sequence 134 AA;
Query March 92.0%; Score 231; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TPQOKYQRLHVEVQLTTEVEKIKTYVESATEERLTPVLLAKQALAL 52
Db 1 TPQOKYQRLHVEVQLTTEVEKIKTYVESATEERLTPVLLAKQALAL 48
RESULT 9
ABP52968
ID ABP52968 standard; peptide; 22 AA.
XX
XX
XX ABP52968;
XX
XX 05-NOV-2002 (first entry)
XX
XX
XX Cellular proliferation inhibitor related peptide SEQ ID NO:3.
XX
XX
XX Cellular proliferation inhibition; cytostatic; anti-inflammatory; cancer;
XX p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
XX sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
XX glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
XX glandular disorder; macrophagal disorder; epithelial disorder;
XX stromal disorder; blastocoelec disorder; angiogenic disorder;
XX immunologic disorder.
XX
XX
XX Homo sapiens.
XX
XX OS Mus musculus.
XX
XX OS Synthetic.
XX
XX
XX WO200264779-A2.
XX
XX
XX 22-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-US001708.
XX
XX 14-FEB-2001; 2001US-00782816.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX
XX Sharp DJ, Rogers GC, Scholey JM;
XX
XX WPI; 2002-657599/70.
XX
XX
XX New peptide inhibitors of p50/dynaminin useful for treating cancer by
XX inhibiting cellular proliferation, e.g. benign or malignant tumors,
XX leukemia and lymphoid malignancies, or inflammatory, angiogenic and
XX immunologic disorders.
XX
XX
XX Claim 1; Page 29; 55pp; English.
XX
XX
XX The present invention describes an isolated peptide (I) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (1) have cytostatic and anti-inflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and

CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 22 AA;

Query Match 45.0%; Score 113; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVKETPOOKYORLLHEVQELTT 22
|||
Db 1 GVKETPOOKYORLLHEVQELTT 22

RESULT 10
ABP52969
ID ABP52969 standard; peptide; 21 AA.

XX AC ABP52969;

XX DT 05-NOV-2002 (first entry)

XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:4.

XX KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.

XX OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

XX PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PF 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Sharp DJ, Rogers GC, Scholey JM;

XX DR WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

XX CC The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (I) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumours); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoeleic disorders; and

CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 21 AA;

Query Match 42.6%; Score 107; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKETPOOKYORLLHEVQELTT 22
|||
Db 1 VKETPOOKYORLLHEVQELTT 21

RESULT 11
ABP52970
ID ABP52970 standard; peptide; 20 AA.

XX AC ABP52970;

XX DT 05-NOV-2002 (first entry)

XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:5.

XX KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoeleic disorder; angiogenic disorder;
KW immunologic disorder.

XX OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

XX PN WO200264779-A2.

XX PD 22-AUG-2002.

XX PF 21-JAN-2002; 2002WO-US001708.

XX PR 14-FEB-2001; 2001US-00782816.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Sharp DJ, Rogers GC, Scholey JM;

XX DR WPI; 2002-657599/70.

XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

XX PS Claim 1; Page 29; 55pp; English.

XX CC The present invention describes an isolated peptide (II) comprising or
XX having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
XX sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
XX terminal extensions. (II) have cytostatic and antiinflammatory activities
XX and can be used as p50/dynaminin inhibitors and in gene therapy. The
XX peptides, nucleic acid molecules and methods from the present invention
XX are useful for treating cancer by inhibiting cellular proliferation, such
XX as benign or malignant tumors (renal, liver, kidney, bladder, breast,
XX gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
XX thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
XX neck tumours); leukemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic and other glandular,
XX macrophagal, epithelial, stromal and blastocoeleic disorders; and
XX inflammatory, angiogenic and immunologic disorders. The present sequence
XX represents a peptide that can be N-terminally added to (P1)

SQ Sequence 20 AA;
Query Match 41.0%; Score 103; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 KETPOOKYORLLHVEQELTT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KETPOOKYORLLHVEQELTT 20
RESULT 12
ABP52966
ID ABP52966 standard; peptide, 23 AA.
XX AC ABP52966;
XX DT 05-NOV-2002 (first entry)
XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:1.
XX KM Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoelec disorder; angiogenic disorder;
KM immunologic disorder.
XX OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX FT Key Location/Qualifiers
FT Misc-difference 22 /label="Leu, Val
FT /note="Leu in humans and Val in Mus musculus"
XX PN WO200264779-A2.
XX PD 22-AUG-2002.
XX PF 21-JAN-2002; 2002WO-US001708.
XX PR 14-FEB-2001; 2001US-00782816.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Sharp DJ, Rogers GC, Scholey JM;
XX DR WPI; 2002-657599/70.
XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.
XX PS Claim 1; Page 29; 55pp; English.
XX CC The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoelec disorders; and
CC inflammatory, angiogenic and immunologic disorders

XX SQ Sequence 23 AA;
Query Match 41.0%; Score 103; DB 5; Length 23;
Best Local Similarity 95.7%; Pred. No. 5.3e-05;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 23 EVEKIKTTVKESATBEKLTPLYL 45
| | | | | | | | | | | | | | | | | | | | | |
Db 1 EVEKIKTTVKESATBEKLTPLYL 23
RESULT 13
ABP52971
ID ABP52971 standard; peptide, 19 AA.
XX AC ABP52971;
XX DT 05-NOV-2002 (first entry)
XX DE Cellular proliferation inhibitor related peptide SEQ ID NO:6.
XX KM Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KM p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KM sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KM glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KM glandular disorder; macrophagal disorder; epithelial disorder;
KM stromal disorder; blastocoelec disorder; angiogenic disorder;
KM immunologic disorder.
XX OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX PN WO200264779-A2.
XX PD 22-AUG-2002.
XX PF 21-JAN-2002; 2002WO-US001708.
XX PR 14-FEB-2001; 2001US-00782816.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Sharp DJ, Rogers GC, Scholey JM;
XX DR WPI; 2002-657599/70.
XX PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.
XX PS Claim 1; Page 29; 55pp; English.
XX CC The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (1) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoelec disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)
SQ Sequence 19 AA;

Query Match 39.0%; Score 96; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ETPOOKYORLLHVEQLTT 22
| | | | | | | | | | | | | | | | | | | | | |
DB 1 TPPOOKYORLLHVEQLTT 19

RESULT 14

ABP52972
ID ABP52972 standard; peptide; 18 AA.

AC ABP52972;

DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:7.

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoealic disorder; angiogenic disorder;
KW immunologic disorder.

OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

PN WO200264779-A2.

PD 22-AUG-2002.

PF 21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

PA (REGC) UNIV CALIFORNIA.

P1 Sharp DJ, Rogers GC, Scholey JM;

WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

PS Claim 1; Page 29; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (I) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoealic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 18 AA;

Query Match 37.1%; Score 93; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPPOOKYORLLHVEQLTT 22
| | | | | | | | | | | | | | | | | | | | | |
DB 1 TPPOOKYORLLHVEQLTT 18

RESULT 15

ABP52973
ID ABP52973 standard; peptide; 17 AA.

AC ABP52973;

DT 05-NOV-2002 (first entry)

DE Cellular proliferation inhibitor related peptide SEQ ID NO:8.

KW Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer;
KW p50 inhibitor; dynaminin inhibitor; gene therapy; tumour; carcinoma;
KW sarcoma; glioblastoma; leukemia; lymphoid malignancy; neuronal disorder;
KW glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
KW glandular disorder; macrophagal disorder; epithelial disorder;
KW stromal disorder; blastocoealic disorder; angiogenic disorder;
KW immunologic disorder.

OS Homo sapiens.
OS Mus musculus.
OS Synthetic.

PN WO200264779-A2.

PD 22-AUG-2002.

PF 21-JAN-2002; 2002WO-US001708.

PR 14-FEB-2001; 2001US-00782816.

PA (REGC) UNIV CALIFORNIA.

P1 Sharp DJ, Rogers GC, Scholey JM;

WPI; 2002-657599/70.

PT New peptide inhibitors of p50/dynaminin useful for treating cancer by
PT inhibiting cellular proliferation, e.g. benign or malignant tumors,
PT leukemia and lymphoid malignancies, or inflammatory, angiogenic and
PT immunologic disorders.

PS Claim 1; Page 29; 55pp; English.

CC The present invention describes an isolated peptide (I) comprising or
CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-
CC terminal extensions. (I) have cytostatic and antiinflammatory activities
CC and can be used as p50/dynaminin inhibitors and in gene therapy. The
CC peptides, nucleic acid molecules and methods from the present invention
CC are useful for treating cancer by inhibiting cellular proliferation, such
CC as benign or malignant tumors (renal, liver, kidney, bladder, breast,
CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and
CC neck tumors); leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoealic disorders; and
CC inflammatory, angiogenic and immunologic disorders. The present sequence
CC represents a peptide that can be N-terminally added to (P1)

XX Sequence 17 AA;

Query Match 35.1%; Score 88; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PPOOKYORLLHVEQLTT 22
| | | | | | | | | | | | | | | | | | | | | |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:43:09 ; Search time 18.9091 Seconds
(without alignments)
264.596 Million cell updates/sec

Title: 09782816-3-1-22

Sequence: 1 GKETPOOKYQRLHNEVQEL.....ESATREKLTPTVLAKQIAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.5	27.7	804	2	TJ32864
2	68	27.1	1742	2	T49451
3	67.5	26.9	1325	2	S16129
4	67	26.7	1287	2	TJ2235
5	67	26.7	2481	2	D80011
6	66	26.3	393	2	T04957
7	66	26.3	866	2	C71509
8	65.5	26.1	1837	2	T41023
9	64	25.5	210	2	B84499
10	63.5	25.3	163	2	S69518
11	63.5	25.3	374	2	D70391
12	63	25.1	281	2	F75216
13	63	25.1	314	2	F90577
14	62.5	24.9	1281	2	JC5368
15	62	24.7	296	2	TJ2222
16	62	24.7	2469	2	H36812
17	61	24.3	442	2	C95070
18	61	24.3	442	2	A97938
19	60.5	24.1	819	2	AC2029
20	60.5	24.1	1214	2	JC2069
21	60	23.9	523	2	S06920
22	60	23.9	695	2	H72243
23	59.5	23.7	279	2	D71453
24	59.5	23.7	665	2	S62328
25	59	23.5	112	2	G72645
26	59	23.5	239	2	D84004
27	59	23.5	550	2	G85436
28	59	23.5	611	2	B90543
29	59	23.5	782	2	A34219

30	59	23.5	951	2	T45726	hypothetical prote
31	59	23.5	2101	2	A42184	nuclear mitotic ap
32	58.5	23.3	154	2	T25602	hypothetical prote
33	58.5	23.3	821	2	A12417	hypothetical prote
34	58	23.1	302	2	T01615	hypothetical prote
35	58	23.1	319	2	T25666	hypothetical prote
36	58	23.1	623	2	A48315	hypothetical prote
37	58	23.1	630	2	D97992	lamin IIF - Africa
38	58	23.1	677	2	T22333	hypothetical prote
39	58	23.1	707	2	S78538	histidine ammonia-
40	58	23.1	727	2	AD2188	site-specific reco
41	58	23.1	740	2	G95153	hypothetical prote
42	58	23.1	978	2	A70387	neuraminidase, pro
43	58	23.1	2139	2	T18286	conserved hypotet
44	58	23.1	2422	2	T12687	myosin heavy chain
45	57.5	22.9	237	2	C87656	ALK protein homolo
						GGDEF family prote

ALIGNMENTS

RESULT 1
TJ32864
hypothetical protein ZK484.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: TJ32864
R:Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid ZK484.
A:Reference number: Z21237
A:Accession: TJ32864
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-804 <MUR>
A:Cross-references: UNIPROT:Q95X56; EMBL:AF040659; PIDD:AA095062.1; GSPDB:GN00019; CESP:
A:Experimental source: strain Bristol N2; clone ZK484
C:Genetics:
A:Gene: CESP:ZK484.4
A:Map position: 1
A:Insertions: 52/1; 113/1; 162/3; 201/3; 248/2; 346/1; 433/2; 464/3; 565/3; 628/2; 646/3; 7
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK484.4

Query Match 27.7%; Score 69.5; DB 2; Length 804;
Best Local Similarity 34.4%; Pred. No. 20;
Matches 22; Conservative 10; Mismatches 19; Indels 13; Gaps 3;

Oy 2 VKETPOOKYQRLHNEVQELTVE-----KTKT-TVESATRE-KLTPVLAKQ 48
Db 366 VEDTPDERKYQKTKYVEIENNEDEDEIGASTSKRKTVTIKKEIDEVKOTPAKURA 425

Oy 49 LAAL 52
Db 426 SAKL 429

RESULT 2
T49451
kinesin-like protein Kif21a related protein [imported] - Neurospora crassa
N:Alternate names: protein B14D6.30
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
R:Schulte, U.; Algn, V.; Hohnsiegel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49451
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1742 <SCH>
A:Cross-references: UNIPROT:Q8X0C5; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.30
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:

A:Gene: NCSP:BI4D6.30
A:Map position: 6
A:Introns: 58/1; 166/1; 267/3; 1543/3

Query Match 27.1%; Score 68; DB 2; Length 1742;
Best Local Similarity 36.6%; Pred. No. 66;
Matches 15; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 7 QOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAK 47
Db 950 EKKQETLDVWEKTEIKAKQALSVESISRTSTPVIIRK 990

RESULT 3
S16129

dyein-associated protein, 150K, cytosolic - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S16129
R:Holzbaur, E.L.F.; Hammarback, J.A.; Paschal, B.M.; Kravt, N.G.; Pfeister, K.K.; Vallee
Nature 351, 579-583, 1991
A:Title: Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophila
A:Reference number: S16129; MUID:91260877; PMID:1828535
A:Accession: S16129
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1325 <KKV>
A:Cross-references: UNIPROT:P28023

Query Match 26.9%; Score 67.5; DB 2; Length 1325;
Best Local Similarity 34.7%; Pred. No. 56;
Matches 17; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

Qy 1 GVKEPQKRYORLHVEVQLTTEVEKIKTVKESATBEKLPVLLAK 49
Db 314 GAASLQGVVAKERVDLTDLILKAIHEKSGDAASYOL-KOL 361

RESULT 4
T22235

hypothetical protein F45G2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22235
R:Lindsay, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19535
A:Accession: T22235
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1287 <WLL>
A:Cross-references: UNIPROT:O62245; EMBL:Z93382; PIDD:CAM07612.1; GSPDB:GN00021; CESP:F4
A:Experimental source: clone F45G2
C:Genetics:
A:Gene: CESP:F45G2.3
A:Map position: 3
A:Introns: 59/1; 117/3; 153/3; 180/2; 233/2; 341/3; 393/1; 424/2; 551/3; 664/3; 734/3; 8

Query Match 26.7%; Score 67; DB 2; Length 1287;
Best Local Similarity 31.6%; Pred. No. 61;
Matches 18; Conservative 11; Mismatches 18; Indels 10; Gaps 2;

Qy 4 ETPQOKYORLHVEVQLTTEV--EKIKTVKESATBEK-----TPVLLAKOLA 50
Db 1122 EPPPKOKILFVIDDSEFPQEKVKENTKESVAEKVENSNEELKPPILIRKAVS 1178

RESULT 5
D90011

FmtB protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D90011

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D90011
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2481 <KUR>
A:Cross-references: UNIPROT:Q99QR6; GB:BA000018; PIDD:GL3701961; PIDD:BAB43253.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmcB(mrp)

Query Match 26.7%; Score 67; DB 2; Length 2481;
Best Local Similarity 35.1%; Pred. No. 1.2e+02;
Matches 13; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 2 VKETPQOKYORLHVEVQLTTEVEKIKTVKESATBEK 38
Db 1609 IEOTPMASQGEINDAKQEVDTLNQAKTNVDQSTNE 1645

RESULT 6
T04957

hypothetical protein F7J7.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04957
R:Beyan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04957
A:Molecule type: DNA
A:Residues: 1-393 <BEV>
A:Cross-references: UNIPROT:O49567; EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
C:Genetics:
A:Map position: 4
A:Introns: 80/1; 217/3; 264/1; 291/3
A:Introns: F7J7.200

Query Match 26.3%; Score 66; DB 2; Length 393;
Best Local Similarity 38.6%; Pred. No. 21;
Matches 17; Conservative 12; Mismatches 7; Indels 8; Gaps 2;

Qy 3 KETPQOKYORLHVEVQLTTEVEKIKTVKESATBEKLPVLL 45
Db 27 QESTQOTHONLXYKVQ-----KMRSTLXDSDAELKLSPALV 63

RESULT 7
C71509

probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: C71509
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia traci
A:Reference number: A71570; MUID:9900809; PMID:9784136
A:Accession: C71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-866 <ARN>
A:Cross-references: UNIPROT:O84500; GB:AB001322; GB:AB001273; NID:G3328916; PIDD:AA06809
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: POLA
C:Superfamily: DNA-directed DNA polymerase I

Query Match 26.3%; Score 66; DB 2; Length 866;

A;Gene: PAB2181

Query Match 25.1%; Score 63; DB 2; Length 281;
Best Local Similarity 36.6%; Pred. No. 30;
Matches 15; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

Qy 1 GVKE-TPQOKYQRLHVEQELTTEVEKIKTVKESATEEKL 40
Db 119 GIKEVVAEEYKELKKEYEKLKQFEFEYKAKI-EAAEIESL 158

RESULT 13

lipoprotein vaa8 [imported] - Mycoplasma pulmonis (strain UAB CTIP) (fragment)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: F90577
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: F90577
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <KUN>
A:Cross-references: UNIPROT:O98043; GB:AL445566; PID:g14089940; PIDN:CAC13699.1; GSPDB:C
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPu_5260
A:Genetic code: SGC3

Query Match 25.1%; Score 63; DB 2; Length 314;
Best Local Similarity 29.8%; Pred. No. 34;
Matches 14; Conservative 17; Mismatches 10; Indels 6; Gaps 2;

Qy 2 VKETPQOKYQRLHVEQELTTEVEKIKTVKESATEEKL 44
Db 246 ITBEOKAKFKDVIQDARTKQDLTKLEKIKS-EKENIEKKLDPII 290

RESULT 14

JC5368
dynamitin 1 - mouse
N:Alternate names: p150 Glued
C:Species: Mus musculus (house mouse)
C>Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5368
R:Jung, W.; Weber, J.S.; Tokito, M.K.; Holzbaun, E.L.F.; Weisler, M.H.
Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A>Title: Mouse p150Glued (dynamitin 1) cDNA sequence and evaluation as a candidate for th
A:Reference number: JC5368; MUID:97223454; PMID:9070275
A:Accession: JC5368
A:Molecule type: mRNA
A:Residues: 1-1281 <UN>
A:Cross-references: UNIPROT:O08788; GB:U60312; NID:g2104494; PIDN:AAB5773.1; PID:g21044
A:Experimental source: brain
C:Comment: This protein is a member of the oligomeric dynamitin complex that is required
C:Genetics:
A:Gene: Dctn1
A:Map position: 6

Query Match 24.9%; Score 62.5; DB 2; Length 1281;
Best Local Similarity 34.8%; Pred. No. 1.8e+02;
Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Qy 4 ETPOOKYQRLHVEQELTTEVEKIKTVKESATEEKLTPVLI 49
Db 319 ESLQOEVALKRVDELTTDLTKALEIEKSGDGAASYQL-KQL 363

RESULT 15

T32222
C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32222
R:Davidson, S.; Wohldmann, P.; Gillam, B.
Submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T32222.
A:Reference number: 221137

A:Accession: T32222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-296 <DAV>
A:Cross-references: UNIPROT:O17002; EMBL:AF022982; PIDN:AAB69938.1; GSPDB:GN00023; CESP:
A:Experimental source: strain Bristol N2; clone T32222
C:Genetics:
A:Gene: CESP:T32222.7
A:Map position: 5
A:Introns: 67/3

Query Match 24.7%; Score 62; DB 2; Length 296;
Best Local Similarity 31.0%; Pred. No. 40;
Matches 18; Conservative 12; Mismatches 12; Indels 16; Gaps 3;

Qy 3 KETPQOKYQRLHVEQELTTEVEKIKTVKESATEEKLTPVLI 47
Db 132 KKTDOIRNFK--EIEAIRQLEKEVNEEVKQKATLMKTEREKHQKQEKLTPLRLK 186

Search completed: November 3, 2005, 22:04:16
Job time : 20.9091 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 ; Search time 91.4866 Seconds
(without alignments)
291.060 Million cell updates/sec

Title: 09782816-3-1-22

Perfect score: 251
Sequence: 1 GVKETPQOKTQRLHVEQEL.....ESATEBKLPVLAQLAAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	100.0	400	1 DCT2_HUMAN	Q13561 homo sapien
2*	248	98.8	401	1 DCT2_MOUSE	Q93KJ8 mus musculu
3	248	98.8	402	1 O6AYH5	Q6AYH5 rattus norv
4	220	87.6	403	2 O6IRB3	Q6IRB3 xenopus lae
5	213	84.9	403	2 O66J30	Q66J30 xenopus lae
6	211	84.1	338	2 O7ZXV2	Q7ZXV2 xenopus lae
7	177	70.5	402	2 O9PTG6	Q9PTG6 gallus gall
8	177	70.5	405	2 O7T3H1	Q7T3H1 brachydantio
9	76	30.3	402	2 O6IP53	Q6IP53 xenopus lae
10	72.5	28.9	380	2 O9V4Y9	Q9V4Y9 drosophila
11	71	28.3	800	2 O6MVP7	Q6MVP7 neurospora
12	71	28.3	813	2 O7SH14	Q7SH14 neurospora
13	70	27.9	311	2 O9TIV5	Q9TIV5 sulfolobus
14	70	27.9	751	2 O8MOK1	Q8MOK1 drosophila
15	70	27.9	1087	2 O8BBS5	Q8BBS5 drosophila
16	70	27.9	1124	2 O8MOK8	Q8MOK8 drosophila
17	70	27.9	2199	2 O7PUP2	Q7PUP2 anopheles g
18	69.5	27.7	873	2 O9SXS6	Q9SXS6 caenorhabdi
19	69.5	27.7	919	2 O9SXS5	Q9SXS5 caenorhabdi
20	68	27.1	1755	2 O7RVJ1	Q7RVJ1 neurospora
21	68	27.1	1968	2 O8XOC5	Q8XOC5 neurospora
22	67.5	26.9	1868	2 O6BNV2	Q6BNV2 debaromyce
23	67	26.7	455	2 O7ZVF1	Q7ZVF1 brachydantio
24	67	26.7	639	2 O6Z245	Q6Z245 caenorhabdi
25	67	26.7	1795	2 O9LCT9	Q9LCT9 staphylococ
26	67	26.7	2478	2 O9LCH2	Q9LCH2 staphylococ
27	67	26.7	2478	2 O9RL69	Q9RL69 staphylococ
28	67	26.7	2481	2 O99OR6	Q99OR6 staphylococ
29	67	26.7	2481	2 O7A4B1	Q7A4B1 staphylococ
30	66	26.3	393	2 O49567	Q49567 arabidopsis
31	66	26.3	860	2 O7Q0Q9	Q7Q0Q9 anopheles g

32	66	26.3	866	2 O84500	O84500 chlamydia t
33	66	26.3	1022	2 O8TB98	O8TB98 homo sapien
34	65.5	26.1	1837	2 O74424	O74424 schizosach
35	65	25.9	388	2 O7P225	O7P225 anopheles g
36	64.5	25.7	348	2 O8LIT9	O8LIT9 oryza sativ
37	64	25.5	149	2 O9B2S3	O9B2S3 homo sapien
38	64	25.5	188	2 O9UM00	O9UM00 homo sapien
39	64	25.5	188	2 O921I3	O921I3 mus musculu
40	64	25.5	188	2 O6DGM9	O6DGM9 brachydantio
41	64	25.5	210	2 O9SIY3	O9SIY3 arabidopsis
42	64	25.5	230	2 O75545	O75545 homo sapien
43	64	25.5	1227	1 J1P3.DROME	J1P3.DROME
44	64	25.5	1956	2 O9Y2K3	O9Y2K3 drosophila
45	63.5	25.3	163	1 Y012_BPHPI	Y012_BPHPI

ALIGNMENTS

RESULT 1
DCT2_HUMAN
ID DCT2_HUMAN STANDARD: PRT; 400 AA.
AC Q13561; O86YN2; O9BW17;
DT 01-NOV-1997 (Rel. 35, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
DE (p50 dynactin) (DCTN-50) (Dynactin 2).
GN Name=DCTN2; Synonyms=DCTN50;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96178072; PubMed=8647893; DOI=10.1083/jcb.132.4.617;
RA Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;
RT "Molecular characterization of the 50-kD subunit of dynactin reveals
RT function for the complex in chromosome alignment and spindle
RT organization during mitosis."
RL J. Cell Biol. 132:617-633(1996).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, Skin, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rabin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A.C., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE OF 1-384 FROM N.A.
RA Annals J.P., Yu-Lee L.-Y.;
RT "Human 50 kD dynactin subunit, p50 dynactin, isolated from HeLa
RT cells."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 1-13.

CC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbr810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Stees A.,
RA Thomas G.R., Vandekerckhove J.,
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides";
RL Nat. Biotechnol. 21:566-569(2003).
CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in synapse formation
CC during brain development.
CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated
CC with dynein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC
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CC
CC EMBL; U50733; AAC50423.1; -;
DR EMBL; BC000718; AAH09478.1; -;
DR EMBL; BC009468; AAH09468.1; -;
DR EMBL; BC014083; AAH14083.1; -;
DR EMBL; AY189155; AAC34395.1; -;
DR Genem; HGNC:2712; DCTN2.
DR MIM; 607376; -;
DR GO; GO:0005813; C:centrosome; TAS.
DR GO; GO:0005869; C:dynein complex; TAS.
DR GO; GO:0000776; C:kinetochore; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR InterPro; IPR006996; Dyneactin.
DR Pfam; PF04912; Dyneactin; 1.
DR KEGG; dynein; Cytoskeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0
FT DOMAIN 98 131 Coiled coil (Potential).
FT DOMAIN 213 243 Coiled coil (Potential).
FT DOMAIN 378 398 Coiled coil (Potential).
FT CONFLICT 34 34 A -> APAQL (in Ref. 1).
FT CONFLICT 35 35 E -> ELK (in Ref. 3).
FT CONFLICT 381 384 LATV -> PGHS (in Ref. 3).
SQ SEQUENCE 400 AA; 44099 MW; 0A55AB95C0B8270F CRC64;

Query Match 100.0%; Score 251; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 GVKETPOOKYQRLHVEVLTTEVKKITTKVKSITTEKTLTPVLAQOLAL 52
Db 93 GVKETPOOKYQRLHVEVLTTEVKKITTKVKSITTEKTLTPVLAQOLAL 144

RESULT 2
DCT2_MOUSE STANDARD; PRT; 401 AA.
AC 099KJ8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUN-2004 (Rel. 44, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Dyneactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
DE (p50 dyneactin) (DCTN-50) (Dyactin 2) (Growth cone membrane protein
DE 23-48K) (GMP23-48K).
GN Name=Dctn2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA DiCicco L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Garinchi P., Prange C.,
RA Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnarone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek A., Smalins D.E.,
RA Sangerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,
RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP TISSUE=Brain;
RC
RX MEDLINE=9144527; PubMed=9144527; DOI=10.1006/dbnc.1997.6447;
RA Abe T.K., Tanaka H., Iwanga T., Odani S., Kuwano R.;
RT "The presence of the 50-kDa subunit of dyneactin complex in the nerve
RT growth cone";
RL Biochem. Biophys. Res. Commun. 233:295-299(1997).
RN [3]
RP INTERACTION WITH BICD2.
RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
RA Hoogenraad C.C., Akhmanova A., Howell S.A., Dortland B.R.,
RA de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.;
RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-
RT dyneactin pathway by interacting with these complexes";
RL EMBO J. 20:4041-4054(2001).
CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in synapse formation
CC during brain development.
CC -1- SUBUNIT: Subunit of dyneactin, a multiprotein complex associated
CC with dynein (By similarity). Interacts with BICD2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC and membrane-associated forms in neonates. Levels of membrane-
CC associated form are greatly reduced in the adult.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; BC004613; AAH04613.1; -;
DR MGD; MGI:107733; Dctn2.
DR InterPro; IPR006996; Dyneactin.
DR Pfam; PF04912; Dyneactin; 1.
KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0
FT DOMAIN 98 131 Coiled coil (Potential).
FT DOMAIN 214 244 Coiled coil (Potential).
SQ SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940EBC CRC64;

Query Match 98.8%; Score 248; DB 1; Length 401;
Best Local Similarity 98.1%; Pred. No. 9.4e-17;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 52
 DB 93 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 144
 RESULT 3
 ID 06AYH5 PRELIMINARY; PRT; 402 AA.
 AC 06AYH5; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DN Dynactin 2.
 GN Name-dctn2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenman C.M., Schuler G.D.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director AGC Project;
 RA Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC079042; AAT79042.1; -
 DR GO: GO:0005869; C:dynactin complex; IEA.
 DR GO: GO:0007017; P:microtubule-based process; IEA.
 DR InterPro: IPR006996; Dynactin.
 DR Pfam: PF04912; Dynactin; 1.
 SQ SEQUENCE 402 AA; 44148 MW; 55033553A4FB052 CRC64;
 Query Match 98.8%; Score 248; DB 2; Length 402;
 Best Local Similarity 98.1%; Pred. No. 9.4e-17;
 Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 52
 DB 94 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 145
 RESULT 4
 ID 06IRB3 PRELIMINARY; PRT; 403 AA.
 AC 06IRB3; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DN Dcn2-prov protein.
 GN Name-dcn2-prov;
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RA Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC070987; AAT70987.1; -
 DR GO: GO:0005869; C:dynactin complex; IEA.
 DR GO: GO:0007017; P:microtubule-based process; IEA.
 DR InterPro: IPR006996; Dynactin.
 DR Pfam: PF04912; Dynactin; 1.
 SQ SEQUENCE 403 AA; 44828 MW; 9FD158C7C7983062 CRC64;
 Query Match 87.6%; Score 220; DB 2; Length 403;
 Best Local Similarity 84.6%; Pred. No. 6e-14;
 Matches 44; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 OY 1 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 52
 DB 94 GVKETPOOKORLHBEVOELTTEVEKIKTYKESATBEKLTPLVLAQOLAL 145
 RESULT 5
 ID 06GJ30 PRELIMINARY; PRT; 403 AA.
 AC 06GJ30; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DN MGC82128 protein.
 GN Name-MGC82128;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081081; AAH81081.1; -
DR InterPro: IPR006996; Dynamitin.
DR Pfam; PF04912; Dynamitin; 1.
SQ SEQUENCE 403 AA; 44737 MW; 86BE8CEB54325EF3 CRC64;
Query Match 84.9%; Score 213; DB 2; Length 403;
Best Local Similarity 82.7%; Pred. No. 3e-13;
Matches 43; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
OY 1 GVKETPQOKYORLHVEQELTEVEKIKTKTKVESATFEKLTPLVALAKQALAL 52
DB 94 GKMETPQOKYORLHVEQELTEVEKIKTKTKVESATFEKLTPLVALAKQVAVL 145
RESULT 6
O7ZXY2 PRELIMINARY; PRT; 338 AA.
ID O7ZXY2;
AC O7ZXY2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dcch2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044069; AAH44069.1; -
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro: IPR006996; Dynamitin.
DR Pfam; PF04912; Dynamitin; 1.
SQ SEQUENCE 338 AA; 38257 MW; 3346E0F0E644B186 CRC64;
Query Match 84.1%; Score 211; DB 2; Length 338;
Best Local Similarity 86.0%; Pred. No. 4e-13;
Matches 43; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 3 KETPQOKYORLHVEQELTEVEKIKTKTKVESATFEKLTPLVALAKQALAL 52
DB 31 KETPQOKYORLHVEQELTEVEKIKTKTKVESATFEKLTPLVALAKQVAVL 80
RESULT 7
O9PTG6 PRELIMINARY; PRT; 402 AA.
ID O9PTG6;
AC O9PTG6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dynamitin.
GN Name=p50;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20056093; PubMed=10588646;
RA Valetti C., Wetzel D.M., Schrader W., Hasbani M.J., Gill S.R.,
RA Kreis T.E., Schroer T.A.;
RT "Role of dynactin in endocytic traffic: effects of dynactin
RT overexpression and colocalization with CLIP-170.";
RL Mol. Biol. Cell 10:4107-4120(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Schroer T.A., Gill S.R., Hasbani M.J., Crego C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200744; AAF13996.1; -
DR GO; GO:0005869; C:dynactin complex; IEA.

DR GO:0007017; P:microtubule-based process; IEA.
DR InterPro:IPR006996; Dyanmitin.
DR Pfam:PF04912; Dyanmitin; 1.
SQ SEQUENCE 402 AA; 45126 MW; F229C467C630DCB9 CRC64;

Query Match 70.5%; Score 177; DB 2; Length 402;
Best Local Similarity 67.3%; Pred. No. 1.2e-09;
Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 GVKETPOQRYRLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 52
DB 96 GAKETPOQRYRLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 147

RESULT 8

Q7T3H1 PRELIMINARY; PRT; 405 AA.
AC Q7T3H1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Similar to dynactin 2 (p50).
GN ORFNames=zgc:63867;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins S.F., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
RA EMBL; BC053120; AAH53120.1; -
DR ZFIN; ZDB-GENE-040426-1279; zgc:63867.
DR GO; GO:0005869; C:dynactin complex; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro:IPR006996; Dyanmitin.
DR Pfam; PF04912; Dyanmitin; 1.
SQ SEQUENCE 405 AA; 44625 MW; CA00047342500953 CRC64;

Query Match 70.5%; Score 177; DB 2; Length 405;
Best Local Similarity 67.3%; Pred. No. 1.2e-09;
Matches 35; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 GVKETPOQRYRLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 52
DB 96 GAKETPOQRYRLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 147

RESULT 9

Q6IP53 PRELIMINARY; PRT; 402 AA.
AC Q6IP53;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MGCT8949 protein.
GN Name=MGCT8949;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins S.F., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RT Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.,
RT Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
RA EMBL; BC072065; AAH72065.1; -
DR GO; GO:0005874; C:microtubule;
DR GO; GO:0000226; P:microtubule cytoskeleton organization and b. . .; IEA.
DR InterPro:IPR000435; Tektin.
DR Pfam; PF03148; Tektin; 1.
DR PRINTS; PR00511; TEKTN.
SQ SEQUENCE 402 AA; 46535 MW; F173BC48FC0E798A CRC64;

Query Match 30.3%; Score 76; DB 2; Length 402;
Best Local Similarity 46.4%; Pred. No. 16;
Matches 13; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 12 RLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 39
DB 336 RLHVEVQLTTEVEKIKTVKESATEEKLTPVLLAKQAL 363

RESULT 10
Q9V4Y9 PRELIMINARY; PRT; 380 AA.
ID Q9V4Y9

AC Q9V4Y9;
 DT 01-MAY-2000 (TReMBLrel. 13. Created)
 DT 01-MAY-2000 (TReMBLrel. 13. Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28. Last annotation update)
 DN CG8269-PA (L007994p).
 DB Name=Dmn; ORFNames=CG8269;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazey R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Esvangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodet K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei H., Ibegam C.,
 RA Jatalai M., Kalush F., Karpen G.H., Ke Z., Kamison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E.R., Wang A.H., Wang X.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Change M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003835; AAF59034.1; -
 DR EMBL; AY061092; AAL2640.1; -
 DR InAct; Q9V4Y9; -
 DR FlyBase; FBgn0021825; Dmn.
 DR GO; GO:0005869; C:dynactin complex; IEA.
 DR GO; GO:0007017; P:microtubule-based process; IEA.
 DR InterPro; IPR006996; Dymanlin.
 DR Pfam; PF04912; Dymanlin; 1.
 SQ SEQUENCE 360 AA; 41998 MW; CF7E1D3BFF5989C5 CRC64;
 Query Match 28.9%; Score 72.5; DB 2; Length 380;
 Best Local Similarity 48.7%; Pred. No. 34;
 Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 Qy 1 GVKRPQKQYRILHVEQELTTEVEKIKTYKESATEEK 39
 Db 94 GKEKTPVQKCPQLQIEMNELNEVAALQVD-RKVADBEK 131
 RESULT 11
 ID Q6WVP7 PRELIMINARY; PRT; 800 AA.
 AC Q6WVP7;
 DT 05-JUL-2004 (TReMBLrel. 27. Created)
 DT 05-JUL-2004 (TReMBLrel. 27. Last sequence update)
 DE Probable translation elongation factor EF-G, mitochondrial.
 GN Name=Bl6D18.030;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX842625; CAB76249.1; -
 DR GO; GO:0005525; F:GTP binding; IEA.

DR GO:0003746; P:translation elongation factor activity; IEA.
DR GO:0006412; P:protein biosynthesis; IEA.
DR GO:0006414; P:translational elongation; IEA.
DR InterPro: IPR004540; EF-G.
DR InterPro: IPR000640; EF-G.
DR InterPro: IPR009022; EF-G_C.
DR InterPro: IPR005517; EF-G_IV.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR007195; ProCSyn_GTPbind.
DR InterPro: IPR005225; Small GTP.
DR InterPro: IPR009000; Translat_factor.
DR Pfam: PF00679; ERG_C; 1.
DR Pfam: PF03764; ERG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF01144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATNFCT.
DR TIGRFAMs: TIGR00484; EF-G; 1.
DR TIGRFAMs: TIGR00231; small GTP; 1.
DR PROSITE: PS00301; EFACOR_GTP; 1.
DR Elongation factor; GTP-binding; Protein biosynthesis.
KW SEQUENCE 800 AA; 88373 MW; F2A7C425F6D4974A CRC64;

Query Match 28.3%; Score 71; DB 2; Length 800;
Best Local Similarity 26.2%; Pred. No. 1e+02;
Matches 16; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 2 VKETPOQKRYRLHEVOELTTEV-----EKIKTVKESATEEKLTPVLLAKQL 49
DB 306 IKELCEQKRGRLIKLADVDDEIEMFLFEQTPPEQKKAIRRTACTCKFTPLVMGSAI 365

QY 50 A 50
DB 366 A 366

RESULT 12
Q7SH14 PRELIMINARY; PRT; 813 AA.
AC Q7SH14;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02955.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qiu D., Ianakiev P., Pedersen D., Braun E.L., Zeller A., Schulte U.,
RA Selltreimkoff C.P., Kinsey J.A., Braun C.L., Marcotte E., Greenberg D.,
RA Koche G.O., Jedd G., Mewes W.S., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysassels M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.U., Osmann S.A.,
RA Desouza C.C., Glass L., Ozbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Naveis D.O., Alex L.A., Mannhaupt G., Ebohe D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
RL Nature 0.0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX0100006; EAA36106.1; -.
DR HSSP; P13551; IFNM.
DR GO:0005525; F:GTP binding; IEA.

DR GO:0003746; P:translation elongation factor activity; IEA.
DR GO:0006412; P:protein biosynthesis; IEA.
DR GO:0006414; P:translational elongation; IEA.
DR InterPro: IPR004540; EF-G.
DR InterPro: IPR000640; EF-G.
DR InterPro: IPR009022; EF-G_C.
DR InterPro: IPR005517; EF-G_IV.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR007195; ProCSyn_GTPbind.
DR InterPro: IPR005225; Small GTP.
DR InterPro: IPR009000; Translat_factor.
DR Pfam: PF00679; ERG_C; 1.
DR Pfam: PF03764; ERG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF01144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATNFCT.
DR TIGRFAMs: TIGR00484; EF-G; 1.
DR TIGRFAMs: TIGR00231; small GTP; 1.
DR PROSITE: PS00301; EFACOR_GTP; 1.
DR GTP-binding; Hypothetical protein; Protein biosynthesis.
KW SEQUENCE 813 AA; 89810 MW; C9A5093F35B29B05 CRC64;

Query Match 28.3%; Score 71; DB 2; Length 813;
Best Local Similarity 26.2%; Pred. No. 1e+02;
Matches 16; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 2 VKETPOQKRYRLHEVOELTTEV-----EKIKTVKESATEEKLTPVLLAKQL 49
DB 306 IKELCEQKRGRLIKLADVDDEIEMFLFEQTPPEQKKAIRRTACTCKFTPLVMGSAI 365

QY 50 A 50
DB 366 A 366

RESULT 13
Q971V5 PRELIMINARY; PRT; 311 AA.
AC Q971V5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein ST1273.
GN OrderedLocustNames=ST1273;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hasegawa A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamaya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagita M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.",
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000985; BAB6315.1; -.
DR HSSP; P01100; IFOS.
KW Complete proteome; Hypothetical protein.
KW SEQUENCE 311 AA; 37536 MW; 674338A5E031B429 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 311;
Best Local Similarity 35.3%; Pred. No. 50;
Matches 18; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

QY 2 VKETPOQKRYRLHEVOELTTEVEKIKTVKESATEEKLTPVLLAKQLAAL 52
DB 71 IKQLSQKQSLIYVISEIKKEFEQIKNVER---VKETLDPYLQILKKEQL 117

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RESULT 14
ID O8MOKL PRELIMINARY; PRT; 751 AA.
AC O8MOKL;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE l008185p
GN ORFNames=CG10971;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Munhall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phoumenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129439; AAM76181.1; -
DR FlyBase; FBgn0036309; CG10971.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002558; ILMQ.
DR Pfam; PF01608; I_LMEQ; 1.
DR PROSITE; PS50945; I_LMEQ; 1.
SQ SEQUENCE 751 AA; 85362 MW; 7E9BC761ECB8A0 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 751;
Best Local Similarity 44.2%; Pred. No. 1.2e+02;
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

Oy 7 QOKYRLHVEOELTTEVEKIKTYKESATSEKLTPTVLAQOL 49
Db 72 KQVNSQLLETKELTKEINLSIKKNVVE--KKE-TNLLQKQI 110

RESULT 15
ID O8EBS5 PRELIMINARY; PRT; 1087 AA.
AC O8EBS5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG10971-PB.
GN ORFNames=CG10971;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RL MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abt'il J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).

[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537558;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RA "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).

[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Celniker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Beltenok B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

[5]
RN
RP SEQUENCE FROM N.A.
RL FlyBase;
RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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RP SEQUENCE FROM N.A.
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003540; AAF49884.1; -
FLYBase; FBgn0036309; CG10971.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005543; F:phospholipid binding; IEA.
DR InterPro; IPR01417; ANTH.
DR InterPro; IPR001026; Epsin_N.
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DR InterPro; IPR002558; ILMEQ.
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DR Pfam; PF07651; ANTH; 1.
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DR ProDom; PD011820; ILMEQ; 1.
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SQ SEQUENCE 1087 AA; 124298 MW; C83E709907DFE8E8 CRC64;

Query Match 27.9%; Score 70; DB 2; Length 1087;
Best Local Similarity 44.2%; Pred. No. 1.8e+02;
Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

Qy 7 QOKXQRLHVEVQELTTEVEKTKTYKESATEEKLTPVLLAKOL 49
Db 408 KQVNSQLLETKEKELTNEISKIKVNE---KEK-TNLTLOKQI 446

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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:51:39 ; Search time 26.6952 Seconds
(without alignments)
145,410 Million cell updates/sec

Title: 09782816-3-1-22

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
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5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	26.3	142	4	US-09-270-767-43370 Sequence 43370, A
2	64.5	25.7	639	4	US-09-902-540-14908 Sequence 14908, A
3	64	25.5	151	4	US-09-513-999C-7806 Sequence 7806, Ap
4	64	25.5	193	4	US-09-107-532A-5587 Sequence 5587, Ap
5	63	25.1	850	4	US-09-269-858A-8 Sequence 8, Appli
6	63	25.1	851	4	US-09-623-326-43 Sequence 43, Appli
7	62.5	24.9	1270	4	US-09-538-092-1321 Sequence 1321, Ap
8	61.5	24.5	309	4	US-09-248-786A-14974 Sequence 14974, A
9	61	24.3	442	3	US-09-081-689-2 Sequence 2, Appli
10	61	24.3	442	3	US-09-305-984-14 Sequence 14, Appli
11	61	24.3	442	3	US-09-073-541A-14 Sequence 14, Appli
12	61	24.3	442	3	US-09-493-940-14 Sequence 14, Appli
13	61	24.3	442	4	US-09-583-110-5317 Sequence 5317, Ap
14	61	24.3	446	4	US-09-107-433-3720 Sequence 3720, Ap
15	61	24.3	644	1	US-08-487-890A-6 Sequence 6, Appli
16	61	24.3	644	2	US-08-478-435-6 Sequence 6, Appli
17	61	24.3	644	2	US-08-337-483-6 Sequence 6, Appli
18	61	24.3	644	2	US-08-478-373-6 Sequence 6, Appli
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20	61	24.3	644	3	US-08-483-577A-6 Sequence 6, Appli
21	61	24.3	644	3	US-08-897-438-6 Sequence 6, Appli
22	61	24.3	644	3	US-08-637-654-6 Sequence 6, Appli
23	61	24.3	644	3	US-08-649-518-6 Sequence 6, Appli
24	60.5	24.1	87	3	US-09-284-033-3 Sequence 3, Appli
25	60.5	24.1	87	3	US-08-729-834B-3 Sequence 3, Appli
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27	59.5	23.7	424	4	US-09-286-981B-14 Sequence 14, Appli

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36	59	23.5	2101	2	US-08-483-924-4 Sequence 4, Appli
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38	59	23.5	2101	3	PCT-US93-06160-4 Sequence 4, Appli
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42	58.5	23.3	399	3	US-08-729-834B-2 Sequence 2, Appli
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44	58.5	23.3	404	4	US-09-949-016-8325 Sequence 8325, Ap
45	58	23.1	487	3	US-09-724-224-8 Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-270-767-43370
Sequence 43370, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43370
LENGTH: 142
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-43370

Query Match      26.3% Score 66; DB 4; Length 142;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 16; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Oy      1 GVKETPOOKYQRLHVEQELTTEVEXIKITKYK 32
Db      111 GVKETPOOKYQRLHVEQELTTEVEXIKITKYK 142

RESULT 2
US-09-902-540-14908
Sequence 14908, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14908
LENGTH: 639
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-14908

Query Match      25.7% Score 64.5; DB 4; Length 639;
```

Best Local Similarity 31.9%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 12; Indels 9; Gaps 1;

Qy 1 GVKETPOQKXQRLHVEQELTTEVEK-----IKTVKESATEE 38
Db 151 GABAVDEQYQADADVERLTSELEASAKESDGLRTAQLAELEE 197

RESULT 3

US-09-513-999C-7806
Sequence 7806, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7806
LENGTH: 151
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -25...-1
OTHER INFORMATION: score 3.9
OTHER INFORMATION: seq RVGLLLGGGGVYG/SR
FEATURE:
NAME/KEY: UNSURE
LOCATION: 94
OTHER INFORMATION: Xaa=Ile or Lys or Asn or Arg or Ser or Thr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 103
OTHER INFORMATION: Xaa=Glu or Lys
US-09-513-999C-7806

Query Match 25.5%; Score 64; DB 4; Length 151;
Best Local Similarity 40.5%; Pred. No. 3;
Matches 17; Conservative 7; Mismatches 8; Indels 10; Gaps 1;

Qy 9 KYORLHVEQELTTEVEKIKTVKESA-----TEEKU 40
Db 86 KYKRLKAEVKQSKLEKKKETITTSAGRQOKKXIERQBEKU 127

RESULT 4

US-09-107-532A-5587
Sequence 5587, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7110
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5587:

SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...193
SEQUENCE DESCRIPTION: SEQ ID NO: 5587:
US-09-107-532A-5587

Query Match 25.5%; Score 64; DB 4; Length 193;
Best Local Similarity 40.5%; Pred. No. 3.9;
Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

Qy 2 VKETPOQKXQRLHVEQELTTEVEKIKTVKESATEE 38
Db 70 VSEIVEQTEVEILRE--EPTAIEVNVETLIEKTEE 104

RESULT 5

US-09-269-858A-8
Sequence 8, Application US/09269858A
Patent No. 6692932
GENERAL INFORMATION:
APPLICANT: Angerer, Bernhard
APPLICANT: Ankenbauer, Waltraud
APPLICANT: Boehringer, M.
APPLICANT: Bonch-Osmolovskaya, Elizaveta
APPLICANT: Markau, Ursula
APPLICANT: Reiser, Astrid
APPLICANT: Schmitz-Agnefian, Gudrun
APPLICANT: Svetlichny, Vitaly
TITLE OF INVENTION: Thermolabile DNA Polymerase From Anaerocellum Thermophilum
FILE REFERENCE: 4452
CURRENT APPLICATION NUMBER: US/09/269,858A
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: PCT/EP97/05390
PRIOR FILING DATE: 1996-10-03
PRIOR APPLICATION NUMBER: EP/96115877
PRIOR FILING DATE: 1996-10-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 850
TYPE: PRT
ORGANISM: Abecus herberti
US-09-269-858A-8

Query Match 25.1%; Score 63; DB 4; Length 850;
Best Local Similarity 30.9%; Pred. No. 28;
Matches 17; Conservative 15; Mismatches 19; Indels 4; Gaps 2;

Qy 1 GVKETPOOKYORLHE---VOELTTEVEKITVKSATTEBKLPVLLAKOLAL 52
Db 192 GVKIGIKSKAKLBEYSLEIYQNDKIKSIREKLEAGK-DMAFLSKRLATI 245

RESULT 6
US-09-623-326-43
; Sequence 43, Application US/09623326
; Patent No. 6607883
; GENERAL INFORMATION:
; APPLICANT: Frey et al.
; TITLE OF INVENTION: Polymerase Chimerae
; FILE REFERENCE: 4894
; CURRENT APPLICATION NUMBER: US/09/623,326
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: DE 198 10 879.6
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 851
; TYPE: PRT
; ORGANISM: Anaerocellum thermophilum
US-09-623-326-43

Query Match 25.1%; Score 63; DB 4; Length 851;
Best Local Similarity 30.9%; Pred. No. 28;
Matches 17; Conservative 15; Mismatches 19; Indels 4; Gaps 2;

Qy 1 GVKETPOOKYORLHE---VOELTTEVEKITVKSATTEBKLPVLLAKOLAL 52
Db 192 GVKIGIKSKAKLBEYSLEIYQNDKIKSIREKLEAGK-DMAFLSKRLATI 245

RESULT 7
US-09-538-092-1321
; Sequence 1321, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 1321
; LENGTH: 1270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321

Query Match 24.9%; Score 62.5; DB 4; Length 1270;
Best Local Similarity 34.8%; Pred. No. 52;
Matches 16; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Qy 4 ETPQOKYORLHEVOELTTEVEKITVKSATTEBKLPVLLAKOL 49
Db 311 ESLQOEVALKERVDELTTTLEILKATIEKSGDAASSTYOL-KOL 355

RESULT 8
US-09-248-796A-14974
; Sequence 14974, Application US/09248796A

; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14974
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14974

Query Match 24.5%; Score 61.5; DB 4; Length 309;
Best Local Similarity 41.2%; Pred. No. 13;
Matches 14; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

Qy 3 KETPOQ---KYORLHEVOELTTEVEKITVKE 33
Db 271 EETPIQDNPXRILHITDLSPTEDIPTPE 304

RESULT 9
US-09-081-689-2
; Sequence 2, Application US/09081689
; Patent No. 6165992
; GENERAL INFORMATION:
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Throup, John
; APPLICANT: Biswas, Sanjoy
; TITLE OF INVENTION: Histidine Kinase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,347
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 442 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-689-2

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Query Match      24.3%; Score 61; DB 3; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Qy      2 VKETPQCKYQRL-----LHEVOELTTEVEKIKTTVESATEEKLTPVLLAKOL 49
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      200 LKEQINSLYQHLLTVIADLHEKNEAIIQLERKVFELRGASHELKTPLASIKIL 253

RESULT 10
US-09-305-984-14
; Sequence 14, Application US/09305984B
; Patent No. 6331407
; GENERAL INFORMATION:
; APPLICANT: No. 6331407ak, Rodger
; APPLICANT: Toumanen, Elaine
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016N1
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: 60/084,399
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 09/305,984
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-305-984-14

Query Match      24.3%; Score 61; DB 3; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Qy      2 VKETPQCKYQRL-----LHEVOELTTEVEKIKTTVESATEEKLTPVLLAKOL 49
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      200 LKEQINSLYQHLLTVIADLHEKNEAIIQLERKVFELRGASHELKTPLASIKIL 253

RESULT 11
US-09-073-541A-14
; Sequence 14, Application US/09073541A
; Patent No. 6448224
; GENERAL INFORMATION:
; APPLICANT: No. 6448224ak, Rodger
; APPLICANT: Toumanen, Elaine
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016
; CURRENT APPLICATION NUMBER: US/09/073,541A
; CURRENT FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-073-541A-14

Query Match      24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Qy      2 VKETPQCKYQRL-----LHEVOELTTEVEKIKTTVESATEEKLTPVLLAKOL 49
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      200 LKEQINSLYQHLLTVIADLHEKNEAIIQLERKVFELRGASHELKTPLASIKIL 253

RESULT 12
US-09-493-940-14
; Sequence 14, Application US/09493940
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; Patent No. 6630583
; GENERAL INFORMATION:
; APPLICANT: No. 6630583ak, Rodger
; APPLICANT: Toumanen, Elaine
; TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
; FILE REFERENCE: 1340-1-016N1
; CURRENT APPLICATION NUMBER: US/09/493,940
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/084,399
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 09/305,984
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-493-940-14

Query Match      24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Qy      2 VKETPQCKYQRL-----LHEVOELTTEVEKIKTTVESATEEKLTPVLLAKOL 49
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      200 LKEQINSLYQHLLTVIADLHEKNEAIIQLERKVFELRGASHELKTPLASIKIL 253

RESULT 13
US-09-563-110-5317
; Sequence 5317, Application US/09563110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/563,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5317
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-563-110-5317

Query Match      24.3%; Score 61; DB 4; Length 442;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Qy      2 VKETPQCKYQRL-----LHEVOELTTEVEKIKTTVESATEEKLTPVLLAKOL 49
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      200 LKEQINSLYQHLLTVIADLHEKNEAIIQLERKVFELRGASHELKTPLASIKIL 253

RESULT 14
US-09-107-433-3720
; Sequence 3720, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
```

```

1 ADDRESS: GENOME THERAPEUTICS CORPORATION
2 STREET: 100 Beaver Street
3 City: Waltham
4 STATE: Massachusetts
5 COUNTRY: USA
6 ZIP: 02354
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: CD/ROM ISO9660
10 OPERATING SYSTEM: <Unknown>
11 SOFTWARE: <Unknown>
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/107,433
14 FILING DATE: 30-Jun-1998
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 60/ 085131
18 FILING DATE: May 12, 1998
19 APPLICATION NUMBER: 60/051553
20 FILING DATE: July 2, 1997
21
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Arinello, Pamela Denae
24 REGISTRATION NUMBER: 40,489
25 REFERENCE/DOCKET NUMBER: GTC-011
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (781)893-5007
28 TELEFAX: (781)893-8277
29
30 INFORMATION FOR SEQ ID NO: 3720:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 446 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 HYPOTHEICAL: YES
37 ORIGINAL SOURCE:
38 ORGANISM: Streptococcus pneumoniae
39
40 FEATURE:
41 NAME/KEY: misc_feature
42 LOCATION: (B) LOCATION 1...446
43
44 SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
45
46 US-09-107-433-3720
47
48 Query Match 24.3% Score 61; DB 4; Length 446;
49 Basic Local Similarity 33.3%; Fred. No. 23;
50 Matches 18; Conservative 6; Mismatches 24; Indels 6; Gaps 1;
51
52 Oy 2 VKETPQOKYORL-----LHEVOELTEVERKIKTVKESATEBKTPVILAKOL 49
53 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
54 Db 204 LKEQINSYQHLTYIADLHKRNKAILOLEKVKVFLRGASHLKTPLASLKITL 257
55
56 RESULT 15
57 US-08-487-890A-6
58 Sequence 6, Application US/08487890A
59 Patent No. 5708149
60
61 GENERAL INFORMATION:
62 APPLICANT: Loosmore, Sheena
63 APPLICANT: Harkness, Robin
64 APPLICANT: Schryvers, Anthony
65 APPLICANT: Chong, Pele
66 APPLICANT: Gray-Owen, Scott
67 APPLICANT: Yang, Yan-Ping
68 APPLICANT: Murdin, Andrew
69 APPLICANT: Klein, Michel
70 TITLE OF INVENTION: Transferrin Receptor Genes
71 NUMBER OF SEQUENCES: 147
72
73 CORRESPONDENCE ADDRESS:
74 ADDRESSEE: Slim & McBurney
75 STREET: 6th Floor, 330 University Avenue
76 City: Toronto
77 STATE: Ontario
78 COUNTRY: Canada
79 ZIP: M5G 1R7
80
81 COMPUTER READABLE FORM:

```

```

1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.25
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/487,890A
7      FILING DATE: 07-JUN-1993
8      CLASSIFICATION: 435
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 08/175,116
11     FILING DATE: 29-DEC-1993
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER: US 08/148,968
14     FILING DATE: 08-NOV-1993
15     ATTORNEY/AGENT INFORMATION:
16     NAME: Stewart, Michael I
17     REGISTRATION NUMBER: 24,973
18     REFERENCE/DOCKET NUMBER: 1038-466 MTS:jb
19     TELECOMMUNICATION INFORMATION:
20     TELEPHONE: (416) 595-1155
21     TELEFAX: (416) 595-1163
22     INFORMATION FOR SEQ ID NO: 6:
23     SEQUENCE CHARACTERISTICS:
24     LENGTH: 644 amino acids
25     TYPE: amino acid
26     STRANDEDNESS: single
27     TOPOLOGY: linear
28
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Query Match Score 61; DB 1; Length 644;
Best Local Similarity 32.6%; Pred. No. 36;
Matches 15; Conservative 8; Mismatches 17; Indels 6; Gaps 1

Search completed: November 3, 2005, 22:05:56
Job time : 27.6952 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:53:15 ; Search time 93.7112 Seconds
(without alignments)
232.174 Million cell updates/sec

Title: 09782816-3-1-22

Perfect score: 251
Sequence: 1 GVKEETPOOKYORLHVEVQEL.....ESATEBKLPVLAKQALAL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	251	100.0	401	16 US-10-408-765A-1369	Sequence 1369, Ap
2	251	100.0	406	10 US-09-782-816A-53	Sequence 53, Appl
3	251	100.0	465	9 US-09-925-298-676	Sequence 676, App
4	251	100.0	465	14 US-10-102-806-676	Sequence 676, App
5	248	98.8	183	10 US-09-782-816A-54	Sequence 54, Appl
6	248	98.8	224	16 US-10-425-115-315831	Sequence 315831,
7	246	98.0	52	10 US-09-782-816A-51	Sequence 51, Appl
8	231	92.0	134	14 US-10-106-698-6730	Sequence 6730, Ap
9	113	45.0	22	10 US-09-782-816A-3	Sequence 3, Appl
10	107	42.6	21	10 US-09-782-816A-4	Sequence 4, Appl
11	103	41.0	20	10 US-09-782-816A-5	Sequence 5, Appl

	12	103	41.0	23	10	US-09-782-816A-1	Sequence 1, Appl
	13	98	39.0	19	10	US-09-782-816A-6	Sequence 6, Appl
	14	93	37.1	18	10	US-09-782-816A-7	Sequence 7, Appl
	15	88	35.1	17	10	US-09-782-816A-8	Sequence 8, Appl
	16	81	32.3	16	10	US-09-782-816A-9	Sequence 9, Appl
	17	76	30.3	15	10	US-09-782-816A-10	Sequence 10, Appl
	18	72.5	28.9	53	10	US-09-782-816A-52	Sequence 52, Appl
	19	72.5	28.9	380	10	US-09-782-816A-56	Sequence 56, Appl
	20	72.5	28.9	380	20	US-11-097-143-4056	Sequence 4056, Ap
	21	71	28.3	14	10	US-09-782-816A-11	Sequence 11, Appl
	22	70.5	28.1	348	16	US-10-425-115-210465	Sequence 210465,
	23	70.5	28.1	356	15	US-10-425-114-63356	Sequence 63356, A
	24	70	27.9	1087	20	US-11-097-143-22866	Sequence 22866, A
	25	70	27.9	1087	20	US-11-097-143-22869	Sequence 22869, A
	26	68	27.1	2368	9	US-09-815-242-5635	Sequence 5635, Ap
	27	68	27.1	2368	9	US-09-815-242-12389	Sequence 12389, A
	28	67	26.7	2478	9	US-09-815-242-5816	Sequence 5816, Ap
	29	67	26.7	2478	9	US-09-815-242-12967	Sequence 12967, A
	30	67	26.7	2478	17	US-10-470-0488-220	Sequence 220, App
	31	67	26.7	2481	15	US-10-282-122A-43762	Sequence 43762, A
	32	66	26.3	13	10	US-09-782-816A-12	Sequence 12, Appl
	33	66	26.3	386	15	US-10-282-122A-71967	Sequence 71967, A
	34	65.5	26.1	576	15	US-10-424-599-274041	Sequence 274041,
	35	65.5	26.1	1837	15	US-10-369-493-22734	Sequence 22734, A
	36	64.5	25.7	348	16	US-10-437-963-139713	Sequence 139713,
	37	64	25.5	185	16	US-10-842-740-3	Sequence 3, Appl
	38	64	25.5	188	14	US-09-284-320-12	Sequence 12, Appl
	39	64	25.5	188	14	US-10-028-072-2	Sequence 2, Appl
	40	64	25.5	188	14	US-10-140-808-2	Sequence 2, Appl
	41	64	25.5	188	14	US-10-121-049-2	Sequence 2, Appl
	42	64	25.5	188	14	US-10-123-904-2	Sequence 2, Appl
	43	64	25.5	188	14	US-10-140-470-2	Sequence 2, Appl
	44	64	25.5	188	14	US-10-175-746-2	Sequence 2, Appl
	45	64	25.5	188	14	US-10-176-918-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-408-765A-1369
; Sequence 1369, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1369
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-1369

Query Match 100.0%; Score 251; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GVKEETPOOKYORLHVEVQELTTEVEKIKTYKESATEBKLPVLAKQALAL 52
DB 94 GVKEETPOOKYORLHVEVQELTTEVEKIKTYKESATEBKLPVLAKQALAL 145

RESULT 2
US-09-782-816A-53
; Sequence 53, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: U0069.001A
; CURRENT APPLICATION NUMBER: US/09/782.816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-816A-53

Query Match 100.0%; Score 251; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.6e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 52
Db 99 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 150

RESULT 3
US-09-925-298-676
; Sequence 676, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925.298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-676

Query Match 100.0%; Score 251; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 52
Db 158 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 209

RESULT 4
US-10-102-806-676

; Sequence 676, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102.806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-676

Query Match 100.0%; Score 251; DB 14; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 52
Db 158 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 209

RESULT 5
US-09-782-816A-54
; Sequence 54, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: U0069.001A
; CURRENT APPLICATION NUMBER: US/09/782.816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-816A-54

Query Match 98.8%; Score 248; DB 10; Length 183;
Best Local Similarity 98.1%; Pred. No. 1.3e-19;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 52
Db 94 GVKEPPOQKYORLHVEVQELTTEVEKIKTTVKSATSEKLTPLVLAQAL 145

RESULT 6
US-10-425-115-315831

; Sequence 315831, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Placids
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315831
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_51109C.1.pcp
US-10-425-115-315831

Query Match 98.8%; Score 248; DB 16; Length 224;
Best Local Similarity 98.1%; Pred. No. 1.7e-19;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 52
Db 47 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 98

RESULT 7

US-09-782-816A-51
; Sequence 51, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069,001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 44
; OTHER INFORMATION: Xaa = Val or Leu
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-51

Query Match 98.0%; Score 246; DB 10; Length 52;
Best Local Similarity 98.1%; Pred. No. 5e-20;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 52
Db 1 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 52

RESULT 8

US-10-106-698-6730
; Sequence 6730, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6730
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6730

Query Match 92.0%; Score 231; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.1e-18;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 TPQOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 52
Db 1 TPQOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 48

RESULT 9

US-09-782-816A-3
; Sequence 3, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; FILE REFERENCE: UC069,001A
; CURRENT APPLICATION NUMBER: US/09/782,816A
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
; OTHER INFORMATION: musculus.
US-09-782-816A-3

Query Match 45.0%; Score 113; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 22
Db 1 GVKETPOOKYORLHVEOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAL 22

RESULT 10

US-09-782-816A-4
; Sequence 4, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathan M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
; TITLE OF INVENTION: PROLIFERATION

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FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 21
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
US-09-782-816A-4
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Query Match      42.6%; Score 107; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2 VKETPOQKYQRLHVEVQELTT 22
      |||||
Db      1 VKETPOQKYQRLHVEVQELTT 21
```

```
RESULT 11
US-09-782-816A-5
Sequence 5, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
US-09-782-816A-5
```

```
Query Match      41.0%; Score 103; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      3 KETPOQKYQRLHVEVQELTT 22
      |||||
Db      1 KETPOQKYQRLHVEVQELTT 20
```

```
RESULT 12
US-09-782-816A-1
Sequence 1, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 23
```

```
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: UNSURE
LOCATION: 22
OTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: The sequence is a Homo sapiens sequence when Xaa
OTHER INFORMATION: represents Leu and a Mus musculus sequence when
OTHER INFORMATION: Xaa represents Val.
US-09-782-816A-1
```

```
Query Match      41.0%; Score 103; DB 10; Length 23;
Best Local Similarity 95.7%; Pred. No. 0.00015;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      23 EKEKIKTVKESATBEKLTVPYL 45
      |||||
Db      1 EKEKIKTVKESATBEKLTVPYL 23
```

```
RESULT 13
US-09-782-816A-6
Sequence 6, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 19
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
US-09-782-816A-6
```

```
Query Match      39.0%; Score 98; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4 ETPOQKYQRLHVEVQELTT 22
      |||||
Db      1 ETPOQKYQRLHVEVQELTT 19
```

```
RESULT 14
US-09-782-816A-7
Sequence 7, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782.816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 18
TYPE: PRT
ORGANISM: Unknown
FEATURE:
```


OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-7

Query Match 37.1%; Score 93; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPQKQYRLHVEVQLTT 22
|||
Db 1 TPQKQYRLHVEVQLTT 18

RESULT 15
US-09-782-816A-8
Sequence 8, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:

APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathan M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
FILE REFERENCE: UC069,001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 17
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
US-09-782-816A-8

Query Match 35.1%; Score 88; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQKQYRLHVEVQLTT 22
|||
Db 1 PQQKQYRLHVEVQLTT 17

Search completed: November 3, 2005, 22:11:40
Job time : 94.7112 secs

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